

# SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*  
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

\*\*\*\*\*  
**STAFF USE ONLY**

	Type of Search	Vendors and cost where applicable
Searcher: <u>Beverly C 4994</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr.Link _____
Date Completed: <u>08-08-9</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) <u>CGN</u>

**THIS PAGE BLANK (USPTO)**

Sehara Sevan  
09/454223  
Seq. ID 1w/1454 Page 1

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2001, 05:06:59 ; Search time 2474.55 Seconds  
(without alignments)  
9267.790 Million cell updates/sec

Title: us-09-454-223-1  
Perfect score: 1552  
Sequence: 1 gctagcgatccacccagga.....agcagctagacactgtacc 1552

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Database: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents, NA, Main:\*

1: /cgnl\_7/ptodata/1/pna/US0612.COMB.seq.\*  
2: /cgnl\_7/ptodata/1/pna/US0613.COMB.seq.\*  
3: /cgnl\_7/ptodata/1/pna/US0614.COMB.seq.\*  
4: /cgnl\_7/ptodata/1/pna/US0615.COMB.seq.\*  
5: /cgnl\_7/ptodata/1/pna/US0616.COMB.seq.\*  
6: /cgnl\_7/ptodata/1/pna/US0617.COMB.seq.\*  
7: /cgnl\_7/ptodata/1/pna/US0618.COMB.seq.\*  
8: /cgnl\_7/ptodata/1/pna/US0619.COMB.seq.\*  
9: /cgnl\_7/ptodata/1/pna/US0620.COMB.seq.\*  
10: /cgnl\_7/ptodata/1/pna/US0621.COMB.seq.\*  
11: /cgnl\_7/ptodata/1/pna/US0622.COMB.seq.\*  
12: /cgnl\_7/ptodata/1/pna/US0623.COMB.seq.\*  
13: /cgnl\_7/ptodata/1/pna/US0624.COMB.seq.\*  
14: /cgnl\_7/ptodata/1/pna/US0625.COMB.seq.\*  
15: /cgnl\_7/ptodata/1/pna/US0626.COMB.seq.\*  
16: /cgnl\_7/ptodata/1/pna/US0627.COMB.seq.\*  
17: /cgnl\_7/ptodata/1/pna/US0628.COMB.seq.\*  
18: /cgnl\_7/ptodata/1/pna/US0629.COMB.seq.\*  
19: /cgnl\_7/ptodata/1/pna/US0630.COMB.seq.\*  
20: /cgnl\_7/ptodata/1/pna/US0631.COMB.seq.\*  
21: /cgnl\_7/ptodata/1/pna/US0632.COMB.seq.\*  
22: /cgnl\_7/ptodata/1/pna/US0633.COMB.seq.\*  
23: /cgnl\_7/ptodata/1/pna/US0634.COMB.seq.\*  
24: /cgnl\_7/ptodata/1/pna/US0635.COMB.seq.\*  
25: /cgnl\_7/ptodata/1/pna/US0636.COMB.seq.\*  
26: /cgnl\_7/ptodata/1/pna/US0637.COMB.seq.\*  
27: /cgnl\_7/ptodata/1/pna/US0638.COMB.seq.\*  
28: /cgnl\_7/ptodata/1/pna/US0639.COMB.seq.\*  
29: /cgnl\_7/ptodata/1/pna/US0640.COMB.seq.\*  
30: /cgnl\_7/ptodata/1/pna/US0641.COMB.seq.\*  
31: /cgnl\_7/ptodata/1/pna/US0642.COMB.seq.\*  
32: /cgnl\_7/ptodata/1/pna/US0643.COMB.seq.\*  
33: /cgnl\_7/ptodata/1/pna/US0644.COMB.seq.\*  
34: /cgnl\_7/ptodata/1/pna/US0645.COMB.seq.\*  
35: /cgnl\_7/ptodata/1/pna/US0646.COMB.seq.\*  
36: /cgnl\_7/ptodata/1/pna/US0647.COMB.seq.\*  
37: /cgnl\_7/ptodata/1/pna/US0648.COMB.seq.\*  
38: /cgnl\_7/ptodata/1/pna/US0649.COMB.seq.\*  
39: /cgnl\_7/ptodata/1/pna/US0650.COMB.seq.\*  
40: /cgnl\_7/ptodata/1/pna/US0651.COMB.seq.\*  
41: /cgnl\_7/ptodata/1/pna/US0652.COMB.seq.\*  
42: /cgnl\_7/ptodata/1/pna/US0653.COMB.seq.\*  
43: /cgnl\_7/ptodata/1/pna/US0654.COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1552	100.0	1552	US-09-454-223-1	Sequence 1, Appl1
2	1261.6	81.3	1477	US-09-454-223-5	Sequence 5, Appl1
3	798.6	51.5	1574	US-09-454-223-3	Sequence 3, Appl1
4	720.2	46.4	879	US-09-645-926A-1	Sequence 1, Appl1
5	710	45.7	1803	US-09-469-519-31	Sequence 31, Appl1
6	710	45.7	1816	PCT-US01-08655-373	Sequence 373, App
7	710	45.7	1816	PCT-US99-30930-1	Sequence 1, Appl1
8	710	45.7	1816	US-09-470-494A-1	Sequence 1, Appl1
9	710	45.7	1816	US-09-470-494A-1	Sequence 1, Appl1
10	710	45.7	1816	US-09-645-926A-5	Sequence 5, Appl1
11	703.2	45.4	1833	US-09-577-408-4413	Sequence 4413, Ap
12	681.2	43.9	840	US-08-234-580-3	Sequence 3, Appl1
13	681.2	43.9	840	US-08-858-197-3	Sequence 3, Appl1
14	681.2	43.9	840	US-09-388-079-1	Sequence 1, Appl1
15	681.2	43.9	840	US-09-388-079A-1	Sequence 1, Appl1
16	686	42.9	839	US-09-023-655-919	Sequence 919, App
17	657.2	42.3	840	PCT-US94-00786-7	Sequence 7, Appl1
18	657.2	42.3	840	PCT-US94-14767-1	Sequence 1, Appl1
19	657.2	42.3	840	PCT-US97-11956-1	Sequence 1, Appl1
20	657.2	42.3	840	US-07-805-723-10	Sequence 10, Appl1
21	657.2	42.3	840	US-07-969-703A-11	Sequence 11, Appl1
22	657.2	42.3	840	US-07-969-703B-11	Sequence 11, Appl1
23	657.2	42.3	840	US-08-009-258-7	Sequence 7, Appl1
24	657.2	42.3	840	US-08-172-664-1	Sequence 1, Appl1
25	657.2	42.3	840	US-08-215-862-1	Sequence 1, Appl1
26	657.2	42.3	840	US-08-396-230-1	Sequence 1, Appl1
27	657.2	42.3	840	US-08-477-733A-11	Sequence 11, Appl1
28	657.2	42.3	840	US-08-484-624-11	Sequence 11, Appl1
29	657.2	42.3	840	US-08-589-721-7	Sequence 7, Appl1
30	657.2	42.3	840	US-08-677-762-1	Sequence 1, Appl1
31	657.2	42.3	840	US-08-769-819-11	Sequence 11, Appl1
32	657.2	42.3	840	US-08-770-974-11	Sequence 11, Appl1
33	657.2	42.3	840	US-08-770-981-11	Sequence 11, Appl1
34	657.2	42.3	840	US-09-088-913-11	Sequence 11, Appl1
35	657.2	42.3	840	US-09-322-021-11	Sequence 11, Appl1
36	657.2	42.3	840	US-09-322-021A-11	Sequence 11, Appl1
37	657.2	42.3	840	US-09-365-940-11	Sequence 11, Appl1
38	657.2	42.3	840	US-09-387-935-1	Sequence 1, Appl1
39	657.2	42.3	840	US-09-393-618-11	Sequence 11, Appl1
40	657.2	42.3	840	US-09-399-106-11	Sequence 11, Appl1
41	657.2	42.3	840	US-09-430-448-1	Sequence 1, Appl1
42	657.2	42.3	840	US-09-545-993-7	Sequence 7, Appl1
43	657.2	42.3	840	US-09-545-993A-7	Sequence 7, Appl1
44	648.2	41.8	786	US-08-107-353-3	Sequence 3, Appl1
45	648.2	41.8	786	US-08-982-272-1	Sequence 1, Appl1

## ALIGNMENTS

```

RESULT 1
US-09-454-223-1
Sequence 1, Application US/09454223
GENERAL INFORMATION:
APPLICANT: Koriubuth, Richard S
TITLE OF INVENTION: Multimeric forms of CD40L and other TNF family members
FILE REFERENCE: TNFSE-collectin fusion proteins
CURRENT APPLICATION NUMBER: US/09/454,223
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 1
LENGTH: 1552
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (7)..(31)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (88)..(799)
OTHER INFORMATION: Mature murine surfactant protein D including hub
OTHER INFORMATION: region, collagenous portion, and neck, but
FEATURE:
NAME/KEY: misc_feature
LOCATION: (801)..(1546)
OTHER INFORMATION: Human CD40 ligand extracellular region, including
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (32)..(88)
OTHER INFORMATION: Signal peptide from murine surfactant protein D
FEATURE:
NAME/KEY: CDS
LOCATION: (32)..(1444)
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Murine
OTHER INFORMATION: surfactant protein D (without the CDS) fused to
PUBLICATION INFORMATION: the extracellular portion of human CD40L
AUTHORS: Striings, Melanie K.
AUTHORS: Strickbine, L
AUTHORS: Clifford, R N.
AUTHORS: Macduff, B M.
AUTHORS: Sato, T A.
AUTHORS: Maliszewski, C R.
AUTHORS: Fanslow, William C.
TITLE: Recombinant human CD40 ligand stimulates B cell
JOURNAL: J. Exp. Med.
VOLUME: 176
ISSUE: 6
PAGES: 1543-1550
DATE: 1992
RELEVANT RESIDUES: 801 TO 1600
PUBLICATION INFORMATION:
AUTHORS: Motwani, M
TITLE: Mouse surfactant protein-D. cDNA cloning,
VOLUME: 155
ISSUE: 12
PAGES: 5671-5677
DATE: 1995
RELEVANT RESIDUES: 32 TO 800
US-09-454-223-1

```

```

Query Match      100.0%; Score 1552; DB 18; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1552; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gctacgaattccacaggaaggaatcgtacatcgtccctctctcctcgtctgtc 60
DB 1 gctacgaattccacaggaaggaatcgtacatcgtccctctctcctcgtctgtc 60
QY 61 gcttgtaagcccttggaatcttggaaggaaggaagcctctcgaagatcagt 120
DB 61 gcttgtaagcccttggaatcttggaaggaaggaagcctctcgaagatcagt 120
QY 121 acccaacacctgacacctgacatctgtgagcccaacagaagatgctcgtcgtg 180
DB 121 acccaacacctgacacctgacatctgtgagcccaacagaagatgctcgtcgtg 180
QY 181 tgaacggaatgggaagaaagtcacaggggtgagaaggtgatacaggttcgaagacc 240
DB 181 tgaacggaatgggaagaaagtcacaggggtgagaaggtgatacaggttcgaagacc 240
QY 241 tatgggctctcaggttgcaaggccctacaggtccagttggaaccaagagaatgg 300
DB 241 tatgggctctcaggttgcaaggccctacaggtccagttggaaccaagagaatgg 300
QY 301 cctcgtcgcaacctggaaccaagagaagacgttgactaaagtggacccctcgaagctcc 360
DB 301 cctcgtcgcaacctggaaccaagagaagacgttgactaaagtggacccctcgaagctcc 360
QY 361 aggtatctcgttcacgttggaagaaggtccctctggaagcaggggaacataagacc 420
DB 361 aggtatctcgttcacgttggaagaaggtccctctggaagcaggggaacataagacc 420
QY 421 tcaaggcaaacaggtctcctaaagagaagctggcccaagagaagtagtgcctcgg 480
DB 421 tcaaggcaaacaggtctcctaaagagaagctggcccaagagaagtagtgcctcgg 480
QY 481 catgcaaggaatcacagggggcaaaaggtccacagggccccaagggaagaagtccccc 540
DB 481 catgcaaggaatcacagggggcaaaaggtccacagggccccaagggaagaagtccccc 540
QY 541 tgggtgcgaaggagcccaaggaagatgctggaagcagcagaccctgcagctcggctcc 600
DB 541 tgggtgcgaaggagcccaaggaagatgctggaagcagcagaccctgcagctcggctcc 600
QY 601 acaaggagctccagggtcccaaggggccccaagactcaagggggaacagaggtgctccgg 660
DB 601 acaaggagctccagggtcccaaggggccccaagactcaagggggaacagaggtgctccgg 660
QY 661 agacaggaagatcaaaaggtgaagcgggtcccaagcagcgtcgtcgtcgaagcagat 720
DB 661 agacaggaagatcaaaaggtgaagcgggtcccaagcagcgtcgtcgtcgaagcagat 720
QY 721 ggaagccttaaaaggaatacagcgtctagaaggtcctctcccaatacgaagacc 780
DB 721 ggaagccttaaaaggaatacagcgtctagaaggtcctctcccaatacgaagacc 780
QY 781 tgcattgctccctgagtcacataagaagttggaacaagataagaagaaatcttca 840
DB 781 tgcattgctccctgagtcacataagaagttggaacaagataagaagaaatcttca 840
QY 841 tgaagatttgcattcaagaaacgatcacagatgtaacaacaggaagaatccttacc 840
DB 841 tgaagatttgcattcaagaaacgatcacagatgtaacaacaggaagaatccttacc 840
QY 901 cctactgaacgttggaaggaatcaaaagcagtttggaagccttgtaagaagataatgt 960
DB 901 cctactgaacgttggaaggaatcaaaagcagtttggaagccttgtaagaagataatgt 960
QY 961 aaacaaagaggaagcaagaagaacagccttggaatgcaaaaggtgacacgaatcc 1020
DB 961 aaacaaagaggaagcaagaagaacagccttggaatgcaaaaggtgacacgaatcc 1020
QY 1021 tcaattcgcgacatgtcataagtgaggcagcgtaaaacaacatctgttacaagt 1080

```

```

Db 1021 tcaatctgcgcacatgcatcgaagtgaggccagcaagtaaacacatctggtctacagctg 1080
QY 1081 ggtctgaaaaaggtactatcacatctgacacacatctgtcaaccctggaaaatgggaaaca 1140
Db 1081 ggtctgaaaaaggtactatcacatctgacacacatctgtcaaccctggaaaatgggaaaca 1140
QY 1141 gctgacacgtctaaagacaggaagctcatctatctatctctgcccgaagctctctgtccaa 1200
Db 1141 gctgacacgtctaaagacaggaagctcatctatctatctctgcccgaagctctctgtccaa 1200
QY 1201 tcgggaagcttcgagtcgaagctccatctatctagccagcctctgctaagaatcccccgttag 1260
Db 1201 tcgggaagcttcgagtcgaagctccatctatctagccagcctctgctaagaatcccccgttag 1260
QY 1261 atctgagagaatctctctcagaagctgcaaataccacagcttcgcgcaaacctctgggca 1320
Db 1261 atctgagagaatctctctcagaagctgcaaataccacagcttcgcgcaaacctctgggca 1320
QY 1321 acatccatctcctctgggagaggtatttgaaatgcaacacagagctctgggtgtgtctcaa 1380
Db 1321 acatccatctcctctgggagaggtatttgaaatgcaacacagagctctgggtgtgtctcaa 1380
QY 1381 tctgactgctcgaagcgaagctgagccatgagcactgagctcagctctctgtgctactcaa 1440
Db 1381 tctgactgctcgaagcgaagctgagccatgagcactgagctcagctctctgtgctactcaa 1440
QY 1441 actctgaaacagtgctcactctgcaagctgtgtgtgagctgagcgtgagagctctcacaata 1500
Db 1441 actctgaaacagtgctcactctgcaagctgtgtgtgagctgagcgtgagagctctcacaata 1500
QY 1501 cagcagaagcttaagcccaatatacactcccaagagatgtagaacgtgacc 1552
Db 1501 cagcagaagcttaagcccaatatacactcccaagagatgtagaacgtgacc 1552

```

RESULT 2  
 US-09-454-223-5  
 : Sequence 5: Application US/09454223  
 : GENERAL INFORMATION:  
 : APPLICANT: Kornbluth, Richard S  
 : TITLE OF INVENTION: Multimeric forms of CD40L and other TNF family members  
 : FILE REFERENCE: TNF- $\alpha$ -collectin fusion proteins  
 : CURRENT APPLICATION NUMBER: US/09/454,223  
 : CURRENT FILING DATE: 1999-12-09  
 : NUMBER OF SEQ ID NOS: 6  
 : SOFTWARE: PatentIn Ver. 2.1  
 : SEQ ID NO 5  
 : LENGTH: 1477  
 : TYPE: DNA  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Description of Artificial Sequence: Murine  
 : OTHER INFORMATION: surfactant protein D (except CRD) fused to the  
 : OTHER INFORMATION: extracellular domain of murine CD40 ligand  
 : FEATURE:  
 : NAME/KEY: 5'UTR  
 : LOCATION: (7)..(31)  
 : OTHER INFORMATION: 5' UTR from rat surfactant protein D  
 : FEATURE:  
 : NAME/KEY: sig\_peptide  
 : LOCATION: (32)..(88)  
 : OTHER INFORMATION: Signal peptide from murine surfactant protein D  
 : FEATURE:  
 : NAME/KEY: CDS  
 : LOCATION: (32)..(1441)  
 : FEATURE:  
 : NAME/KEY: misc\_recomb  
 : LOCATION: (88)..(799)  
 : OTHER INFORMATION: Mature murine surfactant protein D including hub  
 : OTHER INFORMATION: region, collagenous portion, and neck, but  
 : OTHER INFORMATION: excluding carbohydrate recognition domain (CRD)  
 : FEATURE:

```

: NAME/KEY: misc_feature
: LOCATION: (800)..(1441)
: OTHER INFORMATION: Murine CD40 ligand extracellular region, including
: OTHER INFORMATION: stalk
: PUBLICATION INFORMATION:
: AUTHORS: Molwanl, M
: AUTHORS: White, R A.
: AUTHORS: Guo, N
: AUTHORS: Dowler, L L.
: AUTHORS: Tauber, A I.
: TITLE: Mouse surfactant protein-D. cDNA cloning,
: TITLE: characterization, and gene localization to chromosome
: TITLE: 14.
: JOURNAL: J. Immunol.
: VOLUME: 135
: ISSUE: 12
: PAGES: 5671-5677
: DATE: 1995
: RELEVANT RESIDUES: 32 TO 800
: PUBLICATION INFORMATION:
: AUTHORS: Armitage, R
: TITLE: Molecular and biological characterization of a murine
: JOURNAL: Nature
: VOLUME: 357
: ISSUE: 6373
: PAGES: 80-82
: DATE: 1992
: RELEVANT RESIDUES: 801 TO 1441
: US-09-454-223-5

```

Query Match 81.3%; Score 1261.6; DB 18; Length 1477;

Best Local Similarity 91.4%; Pred. No. 0; Mismatches 124; Indels 3; Gaps 1;

```

Db 1 gctaggaattccaccaggaagcaatctgacatgctgcctctctctcatgctgtctt 60
QY 1 gctaggaattccaccaggaagcaatctgacatgctgcctctctctcatgctgtctt 60
Db 61 gcttgacagccctctgggaatctggagcagaagaatgaaagagcctctcgcaagatcagt 120
QY 61 gcttgacagccctctgggaatctggagcagaagaatgaaagagcctctcgcaagatcagt 120
Db 61 gcttgacagccctctgggaatctggagcagaagaatgaaagagcctctcgcaagatcagt 120
QY 121 acccaacacctgacacctgtcatgtgtagcccaagaagaatgagctcctggtgtgtga 180
Db 121 acccaacacctgacacctgtcatgtgtagcccaagaagaatgagctcctggtgtgtga 180
QY 181 tgaacaggaatggagagagaggtccacaggggtgagaaaggtgtaccaggtttgccagagcc 240
Db 181 tgaacaggaatggagagagaggtccacaggggtgagaaaggtgtaccaggtttgccagagcc 240
QY 241 tatgggacctcagaggtctgcaaggccctacaggttcaggttgaaccacaaaggagaaagg 300
Db 241 tatgggacctcagaggtctgcaaggccctacaggttcaggttgaaccacaaaggagaaagg 300
QY 301 cctctgctgcgaacctgagcccaaggagaaacgttgactcaagtgtgacccctccagacttcc 360
Db 301 cctctgctgcgaacctgagcccaaggagaaacgttgactcaagtgtgacccctccagacttcc 360
QY 361 aggtatctctgctcagcctgggaaaagaaaggtccctctggaagcagggagaaacatagagcc 420
Db 361 aggtatctctgctcagcctgggaaaagaaaggtccctctggaagcagggagaaacatagagcc 420
QY 421 tcaaggaacacaggtctcctaaagagagagctggtgcccacaaaggaaagtagtgcctctgg 480
Db 421 tcaaggaacacaggtctcctaaagagagagctggtgcccacaaaggaaagtagtgcctctgg 480
QY 481 catgcaagatctcagagggcacaagagctccacagggccccaaggaggaagaggtgcctccc 540
Db 481 catgcaagatctcagagggcacaagagctccacagggccccaaggaggaagaggtgcctccc 540
QY 541 tggtgcaagagagcccccaggaatgctgagacagagagacctgcggagcctgcgcgtcc 600

```

```

Db 541 tgggtgcaagagagcccaaggaaatgctggagcagcagcctgcgcgacccgctcc 600
Oy 601 acaggagctccagatgctccagggggcccccagactcaagaaggagagatgtctctgg 660
Db 601 acaggagctccagatgctccagggggcccccagactcaagaaggagagatgtctctgg 660
Oy 661 agacagagaaatcaaaagtgtaaaagcggtctccagacagtgctgtctgagcagcagat 720
Db 661 agacagagaaatcaaaagtgtaaaagcggtctccagacagtgctgtctgagcagcagat 720
Oy 721 ggaagccttaaaagaaataatcacagctctagaggttgctctccctccacactcaagaagc 780
Db 721 ggaagccttaaaagaaataatcacagctctagaggttgctctccctccacactcaagaagc 780
Oy 781 tgaattgtctccctgagtgccatagaggttgagagagtaagaagtaagaagatctca 840
Db 781 tgaattgtctccctgagtgccatagaggttgagagagtaagaagtaagaagatctca 840
Oy 841 tgaagattgtatcatgaaacagatcacagatgcaacacagagaaagatccttacc 840
Db 841 tgaagattgtatcatgaaacagatcacagatgcaacacagagaaagatccttacc 900
Oy 901 ctctacgacgtgtgagagagatcaaaagccagttgaaaggttgagagagataatgtt 960
Db 901 ctctacgacgtgtgagagagatcaaaagccagttgaaaggttgagagagataatgtt 960
Oy 961 aacaaagagagagagagagagagagagagagagagagagagagagagagagagagag 960
Db 961 aacaaagagagagagagagagagagagagagagagagagagagagagagagagag 1020
Oy 1021 tcaattgctgacagatgctcaatgagtgagagcagtaaaacacatctgtgtacagtg 1080
Db 1021 tcaattgctgacagatgctcaatgagtgagagcagtaaaacacatctgtgtacagtg 1080
Oy 1081 ggcctgaaagagagagagagagagagagagagagagagagagagagagagagagag 1077
Db 1078 ggcctgaaagagagagagagagagagagagagagagagagagagagagagagagag 1140
Oy 1141 gctgacgcttaaaagagagagagagagagagagagagagagagagagagagagagag 1137
Db 1138 gctgacgcttaaaagagagagagagagagagagagagagagagagagagagagagag 1200
Oy 1201 tggagagcttgagagagagagagagagagagagagagagagagagagagagagagag 1197
Db 1198 tggagagcttgagagagagagagagagagagagagagagagagagagagagagagag 1260
Oy 1261 attcagagagagagagagagagagagagagagagagagagagagagagagagagag 1257
Db 1258 attcagagagagagagagagagagagagagagagagagagagagagagagagagag 1320
Oy 1321 acaatccatccatccatccatccatccatccatccatccatccatccatccatccatcc 1317
Db 1318 gcaagtcgtccatccatccatccatccatccatccatccatccatccatccatccatcc 1380
Oy 1381 tctgacgtacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1377
Db 1378 cgtgacgtacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1440
Oy 1441 acctgaacagctgacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1437
Db 1438 acctgaacagctgacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1473

```

RESULT 3  
US-09-454-223-3

Sequence 3, Application US/09454223  
GENERAL INFORMATION:  
APPLICANT: Kozubuth, Richard S  
TITLE OF INVENTION: Multimeric forms of CD40L and other TNF family members  
FILE REFERENCE: TNF- $\alpha$ -colicin fusion proteins  
CURRENT APPLICATION NUMBER: US/09/454,223  
CURRENT FILING DATE: 1999-12-09

```

? NUMBER OF SEQ ID NOS: 6
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 3
? LENGTH: 1574
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? NAME/KEY: 5'UTR
? LOCATION: (7)..(31)
? OTHER INFORMATION: 5' UTR taken from rat sequence for surfactant
? FEATURE:
? NAME/KEY: sig_peptide
? LOCATION: (32)..(88)
? OTHER INFORMATION: Signal peptide from murine surfactant protein D
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (32)..(1534)
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (32)..(800)
? OTHER INFORMATION: Murine surfactant protein D including hub region,
? OTHER INFORMATION: collagenous portion, and neck, but excluding
? OTHER INFORMATION: carbohydrate recognition domain (CRD)
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (801)..(1534)
? OTHER INFORMATION: Murine RANKL/TRANCE extracellular region,
? OTHER INFORMATION: including stalk
? PUBLICATION INFORMATION:
? AUTHORS: Molteni, M
? AUTHORS: White, R A
? AUTHORS: Guo, N
? AUTHORS: Dowler, L L
? AUTHORS: Tauber, A I
? AUTHORS: Molteni, M
? TITLE: Mouse surfactant protein-D. cDNA cloning,
? TITLE: Characterization, and gene localization to chromosome
? JOURNAL: J. Immunol.
? VOLUME: 155
? ISSUE: 12
? PAGES: 5671-5677
? DATE: 1995
? RELEVANT RESIDUES: 32 TO 800
? PUBLICATION INFORMATION:
? AUTHORS: Anderson, D M
? TITLE: A homologue of the TNF receptor and its ligand enhance
? JOURNAL: Nature
? VOLUME: 390
? ISSUE: 6656
? PAGES: 175-179
? DATE: 1997
? RELEVANT RESIDUES: 801 TO 1534
US-09-454-223-3

```

Query Match 51.5%; Score 798.6; DB 18; Length 1574;  
Best Local Similarity 98.9%; Pred. No. 1.5e-185;  
Matches 804; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

Oy 1 gctagcaattccacagaaagcaatctgacatgctgctctctccatgcttct 60
Db 1 gctagcaattccacagaaagcaatctgacatgctgctctctccatgcttct 60
Oy 61 gcttgaagccctctggaatctggaagcagaatgaagcctctcgagagatcag 120
Db 61 gcttgaagccctctggaatctggaagcagaatgaagcctctcgagagatcag 120
Oy 121 acccaacacccgagccctgagcagctgtagcccaacagaaagatgagctgctgagc 180
Db 121 acccaacacccgagccctgagcagctgtagcccaacagaaagatgagctgctgagc 180

```

QY 161 tggagcggagatcgagagagagatccacagcggtgctgagaaaggtgatctccaggtcttgcagagacc 240  
 Db 161 tggagcggagatcgagagagagagatccacagcggtgctgagaaaggtgatctccaggtcttgcagagacc 240  
 QY 241 tatcgagcgtcccaagaggtttgcagagggccctacacaggtcccaagcttgcagaccaaagagagaaatcg 300  
 Db 241 tatcgagcgtcccaagaggtttgcagagggccctacacaggtcccaagcttgcagaccaaagagagaaatcg 300  
 QY 301 ctctgcctcgcagaaacctcgcagacaaagagagagaaacgtctgaaactaaagctgaaactcccaagaaacttc 360  
 Db 301 ctctgcctcgcagaaacctcgcagacaaagagagagaaacgtctgaaactaaagctgaaactcccaagaaacttc 360  
 QY 361 aggtatctctcgtctccagctcgcagagaaaggtctccctcgcgcagacagagggagaaataagagacc 420  
 Db 361 aggtatctctcgtctccagctcgcagagaaaggtctccctcgcgcagacagagggagaaataagagacc 420  
 QY 421 tcaaaagcgaacaaacaggtctccataagagagagcgcgggcccgaagagagaaataggtgtctctcg 480  
 Db 421 tcaaaagcgaacaaacaggtctccataagagagagcgcgggcccgaagagagaaataggtgtctctcg 480  
 QY 481 catctcaagagatctctcaaggggcagaaagaggtctccacagggcccccgaagggagaaagagatgcgcc 540  
 Db 481 catctcaagagatctctcaaggggcagaaagaggtctccacagggcccccgaagggagaaagagatgcgcc 540  
 QY 541 tgcgtctgcagagagagcccccagggaaatgctgcgcagacagagaaactgcgcagcttcgcgcgtcc 600  
 Db 541 tgcgtctgcagagagagcccccagggaaatgctgcgcagacagagaaactgcgcagcttcgcgcgtcc 600  
 QY 601 acagggagagcttccaaaggtctccaaagggggcccccagagctccaaagggagacagaggtgtctctcg 660  
 Db 601 acagggagagcttccaaaggtctccaaagggggcccccagagctccaaagggagacagaggtgtctctcg 660  
 QY 661 agacagagagaaatccaaaggtcgaagacgggctctccagaaaggtctcgtctcgcagagcagagat 720  
 Db 661 agacagagagaaatccaaaggtcgaagacgggctctccagaaaggtctcgtctcgcagagcagagat 720  
 QY 721 ggaagcgtctaaagaaagaaactacagcgtctctagaggtctgcctctcccaactatcagaagaagc 780  
 Db 721 ggaagcgtctaaagaaagaaactacagcgtctctagaggtctgcctctcccaactatcagaagaagc 780  
 QY 781 tgcattgtctccctgattgcgcatagaaaggttcga 813  
 Db 781 tgcattgtctccctgattgcgcatagaaaggttcga 813

RESULT 4  
 S-09-645-926A-1  
 : Sequence 1, Application US/09645926A  
 : GENERAL INFORMATION:  
 : APPLICANT: ANUJA, SEEMA  
 : APPLICANT: BONEWALD, LYNDIA  
 : TITLE OF INVENTION: CD40 LIGAND AND CD40 AGONIST COMPOSITIONS AND METHODS OF USE  
 : FILE REFERENCE: 4003.001000  
 : CURRENT APPLICATION NUMBER: US/09/645, 926A  
 : CURRENT FILING DATE: 2000-08-24  
 : PRIOR APPLICATION NUMBER: 60/151,250  
 : PRIOR FILING DATE: 1999-08-27  
 : NUMBER OF SEQ ID NOS: 7  
 : SOFTWARE: PatentIn version 3.0  
 : SEQ ID NO 1  
 : LENGTH: 879  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
 : S-09-645-926A-1

	Query Match	Score	720.2;	DB 25;	Length	879;
	Best Local Similarity	99.68;	Pred	No. 2.3e16;		
	Matches 722;	Conservative	0;	Mismatches	3;	Indels
						Gaps
						0;
QY	795 atgcacatagaagctgtgcacagatagaagatgaaaggaattcttcacgaagaattctg	at	tt	tt	tt	tt
ob	155 atcttcacagaagctgtgcacagaatagaaagaattcttcacgaagaattctg	at	tt	tt	tt	tt
ob	214 atcttcacagaagctgtgcacagaatagaaagaattcttcacgaagaattctg	at	tt	tt	tt	tt

OY	855	tcatyaaaaacgataacagagatgcaacacacagagagaaagatctctatcccttaccggaactg	914
Db	215	tcatyaaaaacgataacagagatgcaacacacacagagagaaagatctctatcccttaccggaactg	274
OY	915	aggaagatcaaaagccaggtttggaagctctgtgaaagataataatgtaaacaaagaggaat	974
Db	275	aggaagatcttaaaagccaggtttggaagctctgtgaaagataataatgtaaacaaagaggaat	334
OY	975	cgaaagaaaaaaacagctcttgaaatgcaaaaagagtgatcatgaatctcnaatctggcgcc	1034
Db	335	cgaaagaaaaaaacagctcttgaaatgcaaaaagagtgatcatgaatctcnaatctggcgcc	394
OY	1035	atgctacaagatgagggccagcagtaaaacaacatctgtgttcacagtggcgctgtaaaaaagat	1094
Db	395	atgctacaagatgagggccagcagtaaaacaacatctgtgttcacagtggcgctgtaaaaaagat	454
OY	1095	actataccatgagcgcaacaacactgtgtcaacccctggaaaatgaggaaaacagctgacggttaaaa	1154
Db	455	actataccatgagcgcaacaacactgtgtcaacccctggaaaatgaggaaaacagctgacggttaaaa	514
OY	1155	gacaaagacatctatataatctatgcccgaagtcacactctgtctccaaatcgaggagaactcgaa	1214
Db	515	gacaaagacatctatataatctatgcccgaagtcacactctgtctccaaatcgaggagaactcgaa	574
OY	1215	gtcaagactccatttctaaagccagcctctgtgctaaagtcccccggtagatctgaaagaaatct	1274
Db	575	gtcaagactccatttctaaagccagcctctgtgctaaagtcccccggtagatctgaaagaaatct	634
OY	1275	tactcagagctgcaaaatacccaagttccgcccacaaactctggggcacaacaaatccatctaat	1334
Db	635	tactcagagctgcaaaatacccaagttccgcccacaaactctggggcacaacaaatccatctaat	694
OY	1335	tggagaggaattattgaattgcaaacagaggtgctgtgttctgtaattgagatcgatccaa	1394
Db	695	tggagaggaattattgaattgcaaacagaggtgctgtgttctgtaattgagatcgatccaa	754
OY	1395	ggcaagatgaaacgaatggcactgtgcttcacagctcccttggcttaatacnaaactctgaacagtg	1454
Db	755	ggcaagatgaaacgaatggcactgtgcttcacagctcccttggcttaatacnaaactctgaacagtg	814
OY	1455	caactctgacagctgtgtgtgagagctgaaacgctgggaatctcataatacagacagagcttaa	1514
Db	815	caactctgacagctgtgtgtgagagctgaaacgctgggaatctcataatacagacagagcttaa	874
OY	1515	ggccca 1519	
Db	875	ggcca 879	

```

: RESULT 5
: US-09-469-519-31
: Sequence 31, Application US/09469519
: GENERAL INFORMATION:
: APPLICANT: Thomson, Angus W
: APPLICANT: Liu, Lina
: APPLICANT: Lotze, Michael T
: TITLE OF INVENTION: GENETICALLY-MODIFIED ANTIGEN PRESENTING CELLS FOR THER
: TITLE OF INVENTION: INDUCTION OF IMMUNOTOLERANCE AND METHODS THEREOF
: FILE REFERENCE: UPT-003
: CURRENT APPLICATION NUMBER: US/09/469,519
: CURRENT FILING DATE: 1999-12-22
: EARLIER APPLICATION NUMBER: 60/113766
: EARLIER FILING DATE: 1998-12-23
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 31
: LENGTH: 1803
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (46)..(831)

```

|||||  
|||cagagctgcaataccccaagtccgcacaacttgcggaacaaatccattcat 1334

```

RESULT 6
PCT-US01-08655-373
; Sequence 373, Application PC/TUS0108655
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-065
; CURRENT APPLICATION NUMBER: PCT/US01/08655
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/668,317
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/695,783
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 09/728,628
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/783,066
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 09/816,828
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 584
; SOFTWARE: Custom
; SEQ ID NO 373
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-08655-373

Query Match          45.7%; Score 710; DB 1; Length 1816;
Best Local Similarity 98.6%; Pred. No. 9,5e-164;
Matches 716; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 795 atggccatagaaggttgcagaagatagaagatgaagaagaaatcttcataagatttgat 854
DB 173 atctcatagaagttgacagatagaagaatgaagaatcttcataagatttgat 232
QY 855 loatbaaagcatcagaagatgcaacacagagagaagatccctatccctactgaactgtg 914
DB 233 tcatgaagaacgatacagaagatgcaacacagagagaagatccctatccctactgaactgtg 914
QY 915 agggagattaaagccagtttgaagcttctgaaggtatataatgtttaacaacaagaggaga 974
DB 293 agggagattaaagccagtttgaagcttctgaaggtatataatgtttaacaacaagaggaga 974
QY 975 cgaagaagaagaacagacttgaatgcaaaaagtgatcagaatccccaatcttgaggcac 1034
DB 353 cgaagaagaagaacagacttgaatgcaaaaagtgatcagaatccccaatcttgaggcac 1034
QY 1035 atgtctaagttagggccagcagtaaaacaacatctgtgttaacgttgagtcgtgaagaagat 1094
DB 413 atgtctaagttagggccagcagtaaaacaacatctgtgttaacgttgagtcgtgaagaagat 1094
QY 1095 actacacatagagcaacacacttggtaaccttggaaatgggaaacagctgaccgttaaaa 1154
DB 473 actacacatagagcaacacacttggtaaccttggaaatgggaaacagctgaccgttaaaa 1154
QY 1155 gacaaggccttatatatatactatgcccagaatgcaccttgcgttcaccaatcgggaagcttga 1214
DB 533 gacaaggccttatatatatactatgcccagaatgcaccttgcgttcaccaatcgggaagcttga 1214
QY 1215 gtcaagctcatattatgagcagccttgctgctaaagtcccccggtagattcagaagaacct 1274
DB 593 gtcaagctcatattatgagcagccttgctgctaaagtcccccggtagattcagaagaacct 1274
QY 1275 tactcaagaagtgaataaccacaagttccgcgaacacttcgggcaacaatccattact 1334
DB 653 tactcaagaagtgaataaccacaagttccgcgaacacttcgggcaacaatccattact 1334

```



```

OY 1335 tggagagagattttgaatttgcacacacaggtctgggtctttgtcaaatgtgactgaatccaa 1394
Db 713 tgggggggggtatcttgaattctgcacacacaggtctctgggtgtctgtccaatgtgactgaatccaa 772
OY 1395 gccaaagtgcacatgcagcctctgctctcaagctctcttctgtgcttaactcaaacctctgaacagtgt 1454
Db 773 gccaaagtgcacatgcagcctctgctctcaagctctcttctgtgcttaactcaaacctctgaacagtgt 832
OY 1455 caccttcgagagctgtgtgtgcagctgcagctgcggagttcttcaataatcacgacacagctctaa 1514
Db 833 caccttcgagagctgtgtgtgcagctgcagctgcggagttcttcaataatcacgacacagcggtta 892
OY 1515 gcccaa 1520
Db 893 agccca 898

RESULT 7
PCT-US99-30930-1
: Sequence 1, Application PC/TUS9930930
: GENERAL INFORMATION:
: APPLICANT: University of Vermont and State Agricultural College
: APPLICANT: Newell, Martha Karen
: APPLICANT: Wagner, David H.
: APPLICANT: Newell, Evan
: TITLE OF INVENTION: Use of CD40 Engagement to Alter T Cell
: FILE REFERENCE: 10277/7007WO/HCL/KA
: CURRENT APPLICATION NUMBER: PCT/US99/30930
: CURRENT FILING DATE: 1999-12-22
: EARLIER APPLICATION NUMBER: U.S. 60/114,106
: EARLIER FILING DATE: 1998-12-29
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 1816
: TYPE: DNA
: ORGANISM: Homo Sapiens
: PCT-US99-30930-1

```

Query Match	Similarity	45.7%	Score 710:	DB 1:	Length 1816:
Best Local	Similarity 98.6%	Pred. No. 9.5e-164:			
Matches 716:	Conservative 0:	Mismatches 10:	Indels 0:	Gaps 0:	
QY	795	atggcattatgaaggctctgagacaaatataagaatctgaagaagatctctcatatgaagattctgcat	854		
Db	173	attctcatatgaaggctctgagacaaatataagaatctctcatatgaagattctctgcat	232		
QY	855	tcatatgaataacgaatatcagacagatctgcaaacacacagagagaagaatctcttactcttactgaaactgtg	914		
Db	233	tcatatgaataacgaatatcagacagatctgcaaacacacagagagaagaatctcttactcttactgaaactgtg	292		
QY	915	agggagattatgaagaagccagactcttgaaagcctctgagaaagatataatgtgttaaacaaagaagagaga	974		
Db	293	agggagattatgaagaagccagactcttgaaagcctctgagaaagatataatgtgttaaacaaagaagagaga	352		
QY	975	cgaagaagaagaacacagctcttgaaatctgcaaaaagtgatctcagatccctcaaatctgcggcac	1034		
Db	353	cgaagaagaagaacacagctcttgaaatctgcaaaaagtgatctcagatccctcaaatctgcggcac	412		
QY	1035	atgtcattatgaaggagccagacagatgaataaataatctcgtcttccagtgagggtctgaaaaagat	1094		
Db	413	atgtcattatgaaggagccagacagatgaataaataatctcgtcttccagtgagggtctgaaaaagat	472		
QY	1095	actacacacatgagcacaacactctgtgtaaacctgtgaataaaggggaaacaaagatctgacccgttaaaa	1154		
Db	473	actacacacatgagcacaacactctgtgtaaacctgtgaataaaggggaaacaaagatctgacccgttaaaa	532		
QY	1155	gacaaaggactcttatatatactcattgcccacagatccactctctgtctccaatctgggaagcttcga	1214		
Db	533	gacaaaggactcttatatatactcattgcccacagatccactctctgtctccaatctgggaagcttcga	592		

Qy	1215	gttaaggtccattatctatgccaagcctctgccttaaaagctcccccgttgaattccagagaaact	1274
Db	593	gtcaagagcccaattctatagccagcctctgcctcaaaagctcccccgttgaattccagagaaact	652
Qy	1275	tactcaagatctgcataatacccaagttccgcgcacaacctctgcggtgcacacatactcatctac	1334
Db	653	tactcagagctctgcataatacccaagttccgcgcacaacctctgcggtgcacacatactcatctac	712
Qy	1335	tgggagagagtaatttggaaattgcacaaccagtgctctcggctgtcttgcataatgtaactgtccaa	1394
Db	713	tgggagagagatatttggaaattgcacaaccagtgctctcggctgtcttgcataatgtaactgtccaa	772
Qy	1335	gtccaagtgtgacgaatgagcactgcctctcaagctctcttgcttacttcacaaacctgtgaagaagct	1455
Db	773	gtccaagtgtgacgaatgagcactgcctctcaagctctcttgcttacttcacaaacctgtgaagaagct	832
Qy	1455	caacttcagaagctctgtgtggaaagcttgcacgctctgtggagagcttcataataacagacaggtctaa	1514
Db	833	caacttcagaagctctgtgtggaaagcttgcacgctctgtggagagcttcataataacagacaggtctaa	892
Qy	1515	ggcccaa 1520	
Db	893	ggcccaa 898	

```

: RESULT      8
: US-09-470-494-1
: Sequence 1, Application US/09470494
: GENERAL INFORMATION:
: APPLICANT: Newell, Martha Karen
: APPLICANT: Wagner, David H.
: APPLICANT: Newell, Evan
: TITLE OF INVENTION: Use of CD40 Engagement to Alter T Cell
: TITLE OF INVENTION: Receptor Usage
: FILE REFERENCE: 10277/7007/HCL/KA
: CURRENT APPLICATION NUMBER: US/09/470,494
: CURRENT FILING DATE: 1999-12-22
: EARLIER APPLICATION NUMBER: U.S. 60/114,106
: EARLIER FILING DATE: 1998-12-29
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 1816
: TYPE: DNA
: ORGANISM: Homo Sapiens
: US-09-470-494-1

```

Query Match	Best Local Similarity	45.7%	Score 710:	DB 18:	Length 1816;
Matches 716;	Conservative	0;	Pred. No. 9.5e-164;	Mismatches 10;	Indels 0;
				Gaps 0;	
Oy	795 atgcccataagaagcttggcacaagaatagaaagatctgaagaagatcttcatagaagatttggat	854			
Db	173 atcttcataagaagcttgcagacaagaatagaagaagaaacccctcacygaatttggat	232			
Oy	855 tcatgaaaaacgatacagaagatctgcacaacaggaaagaaagcttcatacctcttaacgtctg	914			
Db	233 tcatgaaaaacgatacagaagatctgcacaacaggaaagaaagcttcatacctcttaacgtctg	292			
Oy	915 aggaagatlaaaagccagctcttgaaagctctcttgtaagagataataatgcttaaacaaagagagga	974			
Db	293 aggaagatlaaaagccagctcttgaaagctctcttgtaagagataataatgcttaaacaaagagagga	352			
Oy	975 cgaagaaagaaacacagctcttgaaatgcaaaaaggtgatcagaatccctcaaaattgcggcac	1034			
Db	353 cgaagaaagaaacacagctcttgaaatgcaaaaaggtgatcagaatccctcaaaattgcggcac	412			
Oy	1035 atgctcatagaagggccgcgcgcgtaaaaacacatcgtcttgacgttgccgtgaaaaagat	1094			
Db	413 atgctcatagaagggccgcgcgcgtaaaaacacatcgtcttgacgttgccgtgaaaaagat	472			

QY 1095 actacacatgagcaacacttgtaaccctggaaatgaggaaacagctgaccgttaaa 1154  
 Db 473 actacacatgagcaacacttgtaaccctggaaatgaggaaacagctgaccgttaaa 1154  
 QY 1155 gacaagactctattatatactatgcccagtcacactctcttccatctgggaagcttga 532  
 Db 533 gacaagactctattatatactatgcccagtcacactctcttccatctgggaagcttga 1214  
 QY 1215 gtaacgtccattatagccagctctgcttaagatcccccggtagatctgagagaatct 592  
 Db 593 gtaacgtccattatagccagctctgcttaagatcccccggtagatctgagagaatct 1274  
 QY 1275 tactaagctctgacaatacccaagctcccgcaaaccttgcggggaacaatccatcaact 652  
 Db 653 tactaagctctgacaatacccaagctcccgcaaaccttgcggggaacaatccatcaact 1334  
 QY 1335 tggagagatatttgatctgcaacagctgcttggtgtgttgcatactgtaactcaaa 1394  
 Db 713 tggagagatatttgatctgcaacagctgcttggtgtgttgcatactgtaactcaaa 1394  
 QY 1395 gccaaatgagcaatgagcactgcttccacgtctcttgcttactcaactctgaaagct 772  
 Db 773 gccaaatgagcaatgagcactgcttccacgtctcttgcttactcaactctgaaagct 1454  
 QY 1455 caacttgcagctgtgtgtgagctgcagctgcggagcttcaataacagcaagcttaa 832  
 Db 833 caacttgcagctgtgtgtgagctgcagctgcggagcttcaataacagcaagcttaa 1514  
 QY 1515 gcccaa 1520  
 Db 893 agccca 898

RESULT 9  
 US-09-470-494A-1  
 ; Sequence 1, Application US/09470494A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Newell, Martha Karen  
 ; APPLICANT: Wagner, David H.  
 ; APPLICANT: Newell, Evan  
 ; TITLE OF INVENTION: Use of CD40 Engagement to Alter T Cell  
 ; FILE REFERENCE: 10277/7007/HCL/KA  
 ; CURRENT APPLICATION NUMBER: US/09/470,494A  
 ; PRIOR FILING DATE: 1989-12-22  
 ; PRIOR APPLICATION NUMBER: U.S. 60/114,106  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1816  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 US-09-470-494A-1

Query Match 45.7%; Score 710; DB 18; Length 1816;  
 Best Local Similarity 98.6%; Pred. No. 9,5e-164;  
 Matches 716; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 795 atggccatagaagttgacagaatagaagatgaagaatcttcataagatttgat 854  
 Db 173 atctcatagaagttgacagaatagaagatgaagaatcttcataagatttgat 854  
 QY 855 tcatgaaacagatagatagatgcaacacagagagaagatccttacttactgactctg 232  
 Db 233 tcatgaaacagatagatagatgcaacacagagagaagatccttacttactgactctg 232  
 QY 915 aggaatataaagcagcttgaagcttggagagataatgttaacaagaagagaga 974  
 Db 293 aggaatataaagcagcttgaagcttggagagataatgttaacaagaagagaga 974  
 QY 975 cgaagaagaagaacagcttgtaaatgcaaaagctgacatcctcctaattgagcgcac 1034

Db 353 cgaagaagaagaacagcttgtaaatgcaaaagctgacatcctcctaattgagcgcac 412  
 QY 1035 atgtcataagtgagcgcagcagtaaaacacatctgtgttaagtggtgtgaaagat 1094  
 Db 413 atgtcataagtgagcgcagcagtaaaacacatctgtgttaagtggtgtgaaagat 1094  
 QY 1095 actaacacatgagcaaacacttgtaaccttggaatgaggaacagctgacgtttaa 472  
 Db 473 actaacacatgagcaaacacttgtaaccttggaatgaggaacagctgacgtttaa 1154  
 QY 1155 gacaagactctattatatactatgcccagtcacactctcttccatctgggaagcttga 532  
 Db 533 gacaagactctattatatactatgcccagtcacactctcttccatctgggaagcttga 1214  
 QY 1215 gtaacgtccattatagccagctctgcttaagatcccccggtagatctgagagaatct 592  
 Db 593 gtaacgtccattatagccagctctgcttaagatcccccggtagatctgagagaatct 1274  
 QY 1275 tactaagctctgacaatacccaagctcccgcaaaccttgcggggaacaatccatcaact 652  
 Db 653 tactaagctctgacaatacccaagctcccgcaaaccttgcggggaacaatccatcaact 1334  
 QY 1335 tggagagatatttgatctgcaacagctgcttggtgtgttgcatactgtaactcaaa 1394  
 Db 713 tggagagatatttgatctgcaacagctgcttggtgtgttgcatactgtaactcaaa 1394  
 QY 1395 gccaaatgagcaatgagcactgcttccacgtctcttgcttactcaactctgaaagct 772  
 Db 773 gccaaatgagcaatgagcactgcttccacgtctcttgcttactcaactctgaaagct 1454  
 QY 1455 caacttgcagctgtgtgtgagctgcagctgcggagcttcaataacagcaagcttaa 832  
 Db 833 caacttgcagctgtgtgtgagctgcagctgcggagcttcaataacagcaagcttaa 1514  
 QY 1515 gcccaa 1520  
 Db 893 agccca 898

RESULT 10  
 US-09-645-926A-5  
 ; Sequence 5, Application US/09645926A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: AHUJA, SEMA  
 ; APPLICANT: BONEWALD, LYNDIA  
 ; TITLE OF INVENTION: CD40 LIGAND AND CD40 AGONIST COMPOSITIONS AND METHODS OF USE  
 ; FILE REFERENCE: 4003,001000  
 ; CURRENT APPLICATION NUMBER: US/09/645,926A  
 ; PRIOR FILING DATE: 2000-08-24  
 ; PRIOR APPLICATION NUMBER: 60/151,250  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 1816  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 US-09-645-926A-5

Query Match 45.7%; Score 710; DB 25; Length 1816;  
 Best Local Similarity 98.6%; Pred. No. 9,5e-164;  
 Matches 716; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 795 atggccatagaagttgacagaatagaagatgaagaatcttcataagatttgat 854  
 Db 173 atctcatagaagttgacagaatagaagatgaagaatcttcataagatttgat 854  
 QY 855 tcatgaaacagatagatagatgcaacacagagagaagatccttacttactgactctg 232  
 Db 233 tcatgaaacagatagatagatgcaacacagagagaagatccttacttactgactctg 232



MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/234,580  
 FILING DATE: 28-APR-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MILLMAN, ROBERT A  
 REGISTRATION NUMBER: 36,217  
 TELEPHONE/DOCKET NUMBER: 1011.1030000/RAM  
 TELEPHONE: (202)371-2500  
 TELEFAX: (202)371-2540  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 840 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 22..807  
 US-08-234-580-3

Query Match: 43.9%; Score 681.2; DB 6; Length 840;  
 Best Local Similarity: 99.6%; Pred. No. 8.8e-157;  
 Matches 683; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 795 atgscatagaaggttgacagaagaagaagaagaatcctgaagatttgat 854  
 155 ATCTTCAATGAGAGGTGGACAGATGAGATGAGAGAGAGAGATCTCATGAGATTGAT 214  
 QY 855 tcatgaagaacatacaagaatgcacacagaagaagaatccttactgaactgtg 914  
 215 TCATGAGAAAGATGACAGAGATGCAACAGAGAGAGAGATCTCATGAGATTGAT 214  
 Db 915 agggatataaagcagtttgaaagccttgtaagagataatgttaaaagaaga 974  
 275 AGGATATTAAGAGCCAGTTTGAAGCTTGTGAAAGATTAATGTTAAACAGAGAGA 334  
 QY 975 cgaagaagaagaacagcttgtaagagataaagaatgcacacagaagaaga 1034  
 335 CGAAGAGAGAGAGAGCTTGAAGCTTGTGAAAGATTAATGTTAAACAGAGAGA 334  
 Db 1035 atgtcataagtgagccagcagaagtaaaacacatctgtttacagtgagc 1094  
 395 ATGTCATTAAGTGAGGCGCAGCAGTAAACACATCTGTGTACAGTGGGCTGAAAAAGAT 454  
 QY 1095 actaacacatgagcaaacacttgtaaccttggaagaaatgggaagaagc 1154  
 455 ACTAACACATGAGCAACACTTGTAACCTGGAAGATGGGAACAGCTGACCGTTAAA 514  
 Db 1155 gacaaagactctatctatctatgcccgaagtaacctctgttccaatcggaagc 1214  
 515 GACAAAGACTCTATCTATCTATGCCCAGAGTCACTCTGTTCATTCGGAGAGCTTCA 574  
 QY 1215 gtaagctccattatgaagcagcctctgctaaagtcctcccggttagatcgagaagaatc 1274  
 575 GTCACACTCCATTATTAACCAAGCCCTCTCTAAAGTCCCGGCTAATTCGAGAGATCT 634  
 QY 1275 tactgaagctgcaataaccacagcttcgccaacacacttgagggaacaacatcattact 1334  
 635 TACTGAAGCTGCAAAATACCCAGCTTCGCCCAAAACCTTGCGGCGAACATCATCTTCACT 694  
 QY 1335 tggagagagatttgaaatgcaacagagtgctcggtgttgtaaatgtgactgaccaa 1394  
 695 TGGGAGAGATTGTAATTCGAACCAAGAGTCTCGGTGTTTGTCAATGTGACTGATCCAA 754  
 QY 1395 gccaaagtgagccatgacatcgtctcaagctcttggttactcaaacactcgacagtg 1454

Db 755 GCCAAGTGAACCATGCGACTGCTTCACGCTCTTGGCTTACTCAAACTGAAACAGTGT 814  
 QY 1455 caccctgagagcctggttggaagctga 1480  
 Db 815 CACCTTGCAAGGCTGTGTGAGAGCTGA 840

## RESULT 13

US-08-858-197-3

Sequence 3, Application US/08858197

GENERAL INFORMATION:

APPLICANT: KEHRY, MERLYN R

APPLICANT: CASTLE, BRIAN E

TITLE OF INVENTION: METHODS FOR PROLIFERATING AND

NUMBER OF SEQUENCES: 4 DIFFERENTIATING B CELLS, AND USES THEREOF

CORRESPONDENCE ADDRESS:

ADDRESS: STERN, KESSLER, GOLDSTEIN &amp; FOX

CITY: WASHINGTON

STATE: D.C.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/858,197

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/234,580

FILING DATE: 28-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: MILLMAN, ROBERT A

REGISTRATION NUMBER: 36,217

REFERENCE/DOCKET NUMBER: 1011.1030000/RAM

TELEPHONE: (202)371-2500

TELEFAX: (202)371-2540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 840 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: CDS

LOCATION: 22..807

US-08-858-197-3

## Query Match

Best Local Similarity: 43.9%; Score 681.2; DB 12; Length 840;

Matches 683; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 795 atgscatagaaggttgacagaagaagaagaagaatcctgaagatttgat 854  
 155 ATCTTCAATGAGAGGTGGACAGATGAGATGAGAGAGAGAGATCTCATGAGATTGAT 214  
 QY 855 tcatgaagaacatacaagaatgcacacagaagaagaatccttactgaactgtg 914  
 215 TCATGAGAAAGATGACAGAGATGCAACAGAGAGAGAGATCTCATGAGATTGAT 214  
 Db 915 agggatataaagcagtttgaaagccttgtaagagataatgttaaaagaaga 974  
 275 AGGATATTAAGAGCCAGTTTGAAGCTTGTGAAAGATTAATGTTAAACAGAGAGA 334  
 QY 975 cgaagaagaagaacagcttgtaagagataaagaatgcacacagaagaaga 1034



TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Penile & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/388,079A  
 FILING DATE: 31-Aug-1999  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mistrock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 5624-251  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212 790-9090  
 TELEFAX: 212 869-8664/9741  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 840 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLETYPE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 22..807  
 US-09-388-079A-1  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Query Match 43.9% Score 681.2; DB 17; Length 840;  
 Best Local Similarity 99.6%; Pred. No. 8.8e-157;  
 Matches 683; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 795 atggtcatalagaagcttgagcaagaatagaagaatgaagaagaaatctcatgaagatttgat 854  
 DB 155 ATCTTCATGAGAGGTTGGACAAAGATAGAGATGAAGAGATCTTCATGAAGATTTGTAT 214  
 QY 855 tcatcaaaacgatcagagatgcacaacagagagaagatcccttacttactgaactgtg 914  
 DB 215 TCATCAAAACGATACAGATGCAACACAGAGAAAGATCTTATCTTACTGAACTGTG 274  
 QY 915 agggatlaaagcagcttgaaagcttggtaagataaagttaaaacaagaaga 974  
 DB 275 AGGAGATTAAAGCGAGTTTGAAGGCTTTGTGAAGATATATGTTAAACAAAGAGAGA 334  
 QY 975 cgaagaagaacacagcttgaatgcacaagaagtgatcagaatcccaattgcggcac 1034  
 DB 335 CGAAGAAAGAAAACACTTGTGAATGCAAAAAGTGATCAGATCTCAAAATTGCCGCAC 394  
 QY 1035 atgtcctaagtgaagccagcagtaaaacaacatctgttacagtggctgaaagaagat 1094  
 DB 395 ATGTCTAATAGTGAGCCAGAGTAAACACATCTGTTCACAGTGGGCTGAAAAAGGAT 454  
 QY 1095 actacaccatgagcaacaacttgtaacctggaaaaatggaaaacagctgaccttaaa 1154  
 DB 455 ACTACACCATGAGCAACACTTGTGAACCTCGAAAAATGGAAACAGCTGACCTTTAAA 514  
 QY 1155 gacaagacctatatactatagccaaagtaacacctctgtccaatcgggaagctcga 1214  
 DB 515 GACAAGCACTCTATTATATATATGCCAAGTCACTTCTGTTCATCGGGAAGCTTGA 574  
 QY 1215 gtcaagctcattatagcagcctctgcctaaagtcctcccgtagattcgagagaatct 1274

DB 575 GTCAAGCTCATTTATAGCCAGCTCTGTGCTAAAGTCCCGGAGTAGTTGAGAGATCT 634  
 QY 1275 tactcagagctgaaataaccacacagctcgcgcaaaccttcgggcaacaatccatcact 1334  
 DB 635 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGGGCAACAATCCATTCAC 694  
 QY 1335 tgggaagatattgaattgcaaccagtgcttcggtgtgttcaatgtgactgtccaa 1394  
 DB 695 TGGGAGAGTATTGAATTGCAACCAAGTCTCGGTGTTTGCATGTGACTGATCCAA 754  
 QY 1395 gccaaagtacgcacatggacactggcttcacgctccttggcttactcaaacctcgaacagtg 1454  
 DB 755 GCCAAGTAGCAGATGCGACAGTGGCTTCACGTCCTTGTGCTTACTCAAACTGTGAACAGTGT 814  
 QY 1455 gaccttgcagagctgtgtgtgagctga 1480  
 DB 815 CACCTTCAGAGCTGTGTGTGAGCTGA 840

Search completed: August 8, 2001, 06:41:33  
 Job time: 5674 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2001, 04:22:54 ; Search time 178.33 Seconds  
(without alignments)  
6847.508 Million cell updates/sec

Title: US-09-454-223-1  
Perfect score: 1552  
Sequence: 1 gctacgcacatccaccacagc.....agccatgtagaactgctacc 1552

Scoring table:  
IDENTITY\_NUC  
Gap 10.0 , Gapext 1.0

Archived: 407432 seqs, 393400832 residues

Total number of hits satisfying chosen parameters: 814864

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents, NA, New: \*  
1: /cgnl\_7/ptodata/2/pna/PCT\_NEW\_COMB\_seq: \*  
2: /cgnl\_7/ptodata/2/pna/US06\_NEW\_COMB\_seq: \*  
3: /cgnl\_7/ptodata/2/pna/US07\_NEW\_COMB\_seq: \*  
4: /cgnl\_7/ptodata/2/pna/US08\_NEW\_COMB\_seq: \*  
5: /cgnl\_7/ptodata/2/pna/US09\_NEW\_COMB\_seq: \*  
6: /cgnl\_7/ptodata/2/pna/US60\_NEW\_COMB\_seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description
1	705.2	45.4	1833 1	Sequence 3489, Ap
2	615.6	39.7	950 5	Sequence 46, Appl
3	615.6	39.7	950 5	Sequence 123, Appl
4	615.6	39.7	950 5	Sequence 323, Appl
5	143.4	9.2	6306 6	Sequence 1151, A
6	133.4	8.6	4840 6	Sequence 1152, A
7	131.8	8.5	6943 6	Sequence 10948, A
8	131.4	8.5	3753 6	Sequence 10472, A
9	131	8.4	9033 6	Sequence 10792, A
10	129.4	8.3	2060 5	Sequence 181, App
11	129.4	8.3	4137 5	Sequence 5037, Ap
12	128.6	8.3	4629 1	Sequence 3887, Ap
13	128.6	8.3	6191 5	Sequence 1637, Ap
14	127.2	8.2	4748 6	Sequence 11304, A
15	127.2	8.2	4796 6	Sequence 10582, A
16	127.2	8.2	5947 6	Sequence 10573, A
17	126.6	8.2	2054 5	Sequence 22, Appl
18	125.6	8.1	2520 5	Sequence 53, Appl
19	123.2	7.9	4149 6	Sequence 104, Appl
20	122.6	7.9	2382 5	Sequence 72, Appl
21	121.2	7.8	4592 6	Sequence 10512, A
22	121.2	7.8	4699 5	Sequence 178, Appl
23	121.2	7.8	5432 6	Sequence 15988, A
24	119.6	7.7	3078 5	Sequence 3964, Ap
25	118.4	7.6	522 5	Sequence 2433, Ap
26	116.6	7.5	1835 6	Sequence 1163, A
27	116.4	7.5	3016 6	Sequence 1163, A

28	116.4	7.5	3876 6	US-60-278-258-10748	Sequence 10748, A
29	115	7.4	1429 5	US-09-898-888-21593	Sequence 21593, A
30	111.4	7.2	511 5	US-09-849-626-1138	Sequence 1138, Ap
31	111	7.2	6766 5	US-09-652-125A-9454	Sequence 9454, Ap
32	110.6	7.1	2683 6	US-60-278-258-10761	Sequence 10761, A
33	110.6	7.1	5318 6	US-60-278-258-10889	Sequence 10889, A
34	110.2	7.1	2375 5	US-09-764-864-232	Sequence 232, App
35	110.2	7.1	4202 5	US-09-808-383-5593	Sequence 5593, Ap
36	110	7.1	2151 6	US-60-278-258-10596	Sequence 10596, A
37	109.4	7.0	5432 6	US-60-278-258-10919	Sequence 10919, A
38	109	7.0	562 5	US-09-808-383-1191	Sequence 1191, Ap
39	108.8	7.0	2073 5	US-09-760-443-581	Sequence 581, Appl
40	108.6	7.0	507 5	US-09-823-301-8145	Sequence 8145, Ap
41	108.6	7.0	2913 6	US-60-278-258-10625	Sequence 10625, A
42	108.4	7.0	587 5	US-09-808-383-3569	Sequence 3569, Ap
43	107.8	6.9	10759 6	US-60-278-258-10426	Sequence 10426, A
44	106.8	6.9	570 5	US-09-808-383-91	Sequence 91, Appl
45	105.2	6.8	3690 6	US-60-260-483-448	Sequence 448, Appl

ALIGNMENTS

RESULT 1  
PCT-US01-14827-3489  
Sequence 3489, Application PC/TUS0114827  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 21272-104  
CURRENT APPLICATION NUMBER: PCT/US01/14827  
CURRENT FILING DATE: 2001-05-16  
PRIOR APPLICATION NUMBER: 09/577,408  
PRIOR FILING DATE: 2000-05-18  
NUMBER OF SEQ ID NOS: 16102  
SOFTWARE: Custom  
SEQ ID NO: 3489  
LENGTH: 1833  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIMILAR  
LOCATION: (57)-(839)  
OTHER INFORMATION: 100% homologous to Homo sapiens CD40 surface  
OTHER INFORMATION: protein/accession number L07414, Smith-Waterman Score=1335.  
PCT-US01-14827-3489  
Query Match 45.4% Score 705.2; DB 1; Length 1833;  
Best Local Similarity 98.2% Pred. No. 5.8e-163;  
Matches 713; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
Query 795 atggcctaaagaggtgtgacagatagaatgaagaatcctcatgaagattgtat 854  
DB 190 atctcatagaagtcgtgcgaagatagaatgaagaatcctcatgaagattgtat 249  
Query 855 tcatgaagaagatagagatgcaacacagaggaagatccttaccatgaactgtg 914  
DB 250 tcatgaagaagatagagatgcaacacagaggaagatccttaccatgaactgtg 309  
Query 915 aggaagatgaagagcagtttgaagcttctgtgaagatataatgttaacaaaggaga 974  
DB 310 aggaagatgaagagcagtttgaagcttctgtgaagatataatgttaacaaaggaga 369  
Query 975 cgaagaaagaaacagcttgaatgcaaaagagatcagaatcctcaatctggcgc 1034  
DB 370 cgaagaaagaaacagcttgaatgcaaaagagatcagaatcctcaatctggcgc 429  
Query 1035 atgtcataagtgagccagcagtaaaacacacatctgtgtacagtggtgtaaaagat 1094  
DB 430 atgtcataagtgagccagcagtaaaacacacatctgtgtacagtggtgtaaaagat 489  
Query 1095 actaacacatgagcaaaactgtgtaacccttggaataatggaacacagctgacctaa 1154

Db 490 actaacccatgagcaacaacttggtaacccctgtgaaaa tgggaaacaagctgcgtttaa 5499

Qy 1155 gacaagaagatctatatactatctatgcgaagtaacctctgttccaatcgggaagcttcga 121

Db 550 gacaagagctcatatatactatctatgcgaagtaacctctctgttccaatcgggaagcttcga 121

Qy 1215 gcaagagctcatatatactatgcagcctctgtcttaagtcccccggtagattgagaatact 1274

Db 610 gtcaagctcccatctatatagcagcctctgtcttaagtcccccggtagattcgaagaatact 1274

Qy 1275 tactcagaagctgcaaatatacccaagctctcggcaaaccttgcgggcaaacatccatctact 1334

Db 670 taccacagagctgcaaatatacccaagctctcggcaaaccttgcgggcaaacatccatctact 1334

Qy 1335 tgggaagagctatttgaattgttaaaccaaggctcctcgggtttgttcaagtgtgactatccaa 1394

Db 730 tgggaagagctatttgaattgttaaaccaaggctcctcgggtttgttcaagtgtgactatccaa 1394

Qy 1395 gccaaagtgaagcaatgcggaactggctcactctcttggctctcctcaaacctcgaaagctt 1454

Db 790 gccaaagtgaagcaatgcggaactggctcactctcttggctctcctcaaacctcgaaagctt 1454

Qy 1455 cacccttcgaagctcgtgtgtggaactgacgctggagagctctcataatacgaagagcttaa 1514

Db 850 cacccttcgaagctcgtgtgtggaactgacgctggagagctctcataatacgaagagcttaa 1514

Qy 1515 gcccaaa 1520

Db 910 agtccaa 915

```

RESULT: 2
US-09-760-481-46
: Sequence 46 Application US/09760481
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PT64
: CURRENT APPLICATION NUMBER: US/09/760,481
: PRIOR FILING DATE: 2001-01-16
: NUMBER OF SEQ ID NOS: 317
: SOFTWARE: Flatlin Ver. 2.0
SEQ ID NO 46
LENGTH: 950
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (42)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (48)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (315)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (840)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (889)
OTHER INFORMATION: n equals a,t,g, or c
US-09-760-481-46

```

```

Query Match          39.7%; Score 615.6; DB 5; Length 950;
Best Local Similarity 96.2%; Pred. No. 3.8e-141;
Matches 657; Conservative 4; Mismatches 16; Indels 6; Gaps 3.
QY 795 atggcattgaaggtctggacaagaatagaagatgaagaagaatctcatgaagatttgat 854
||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```

Db	259	atcttcataagaagcttgagcaagaatagaagatgaagaagatcttcatagaagattctgcat	318
Oy	855	tcatgaanaacgatacagaagaatgacaacaagaagaaagaatctctctctactgaacgtg	914
Db	319	tcatgaaaaacgatacagaagatgacaacacagaagaaagctctctctctactgaacgtg	914
Oy	915	aggagaattaaaagccagctttgaagctcttggaagagataaagcttaacaagaagagaa	974
Db	379	aggagaattaaaagccagctctggaagagctcttggaagagataaagcttaacaagaagagaa	974
Oy	975	cgaagaaagaaagccagctctggaatgcaaaaagtgatcagaatccctcaattcgcgcac	1034
Db	439	cgaagaaagaaagccagctctggaatgcaaaaagtgatcagaatccctcaattcgcgcac	1034
Oy	1035	atgtcataagtgagagccagcagatgaanaacacatctgtgtttacagtggtgcttaaaaagat	1094
Db	499	atgtcataagtgagagccagcagatgaanaacacatctgtgtttacagtggtgcttaaaaagat	1094
Oy	1095	actccacatcagagcaacaacacttgtgtaacctggaagaaatgggnaaacagcttbaacgcttaaaa	1154
Db	559	actccacatcagagcaacaacacttgtgtaacctggaagaaatgggnaaacagcttbaacgcttaaaa	1154
Oy	1155	gacaagagatctatatactatctatgcccagaatgcacctctgttccaaatcggaagacttga	1214
Db	619	gacaagagatctatatactatctatgcccagaatgcacctctgttccaaatcggaagacttga	1214
Oy	1215	gtcaagctccatctatatactatctatgcccagaatgcacctctgttccaaatcggaagacttga	1274
Db	679	gtcaagctccatctatatactatctatgcccagaatgcacctctgttccaaatcggaagacttga	1274
Oy	1275	taccacaagctgcgaatatccacaagcttccgcgaacaaaccttggcggaacaacatccattcaact	1334
Db	739	taccacaagctgcgaatatccacaagcttccgcgaacaaaccttggcggaacaacatccattcaact	1334
Oy	1335	tgggaagagatattgaattgcaacagaagtctctcgtgttgccaatgtgactgatacga	1394
Db	799	tgggaagagatattgaattgcaacagaagtctctcgtgttgccaatgtgactgatacga	1394
Oy	1395	gtccaaagt-gaaccatgagcagcagcttgaagctcttggttaactc-----aaactcgaac	1449
Db	859	gtccaaagt-gaaccatgagcagcagcttgaagctcttggttaactc-----aaactcgaac	1449
Oy	1450	agct-tcaacttcgaagctctgga	1471
Db	919	aggttcacactgcagcgtctg	941

```

RESULT 3
US-09-760-481-123
/ Sequence 123, Application US/09760481
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: Ptz64
/ CURRENT APPLICATION NUMBER: US/09/760,481
/ Prior application data removed - refer to PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 317
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 123
/ LENGTH: 950
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (42)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: SITE
/ LOCATION: (48)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: SITE
/ LOCATION: (815)
/ OTHER INFORMATION: n equals a,t,g, or c

```



```

; NAME/KEY: SITE
; LOCATION: (840)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (889)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-760-481-123

```

```

Query Match          39.7%; Score 615.6; DB 5; Length 950;
Best Local Similarity 96.2%; Pred. No. 3,8e-141;
Matches 657; Conservative 4; Mismatches 16; Indels 6; Gaps 3;

```

```

QY 795 atggcattgaaggtctggacaagatagaagatgaagaatcttcataagatttgcatt 854
DB 259 atcttcattgaaggtctggacaagatagaagatgaagaatcttcataagatttgcatt 318
DB 855 tctcgaagaacgtctgaagatgacacacaggaagaatcttcataagatttgcatt 914
DB 319 tcatgaaaacgatacagagatgacacacaggaagaatcttcataagatttgcatt 378
QY 915 aggaagatcaaaagcagcttgaagctcttggaagataataatgataaacaagaagaga 974
DB 379 aggaagatcaaaagcagcttgaagctcttggaagataataatgataaacaagaagaga 438
QY 975 cgaagaagaagaacagcttgaagatgacacacaggaagaatcttcataagatttgcatt 1034
DB 439 cgaagaagaagaacagcttgaagatgacacacaggaagaatcttcataagatttgcatt 498
QY 1035 atgtcataagttgagcagcagatgaagaacacatctgttatacagtgagctgaagaagat 1094
DB 499 atgtcataagttgagcagcagatgaagaacacatctgttatacagtgagctgaagaagat 558
QY 1095 actacacacatgagcagcagcttgaagcttgaagcttgaagcttgaagcttgaagct 1154
DB 559 actacacacatgagcagcagcttgaagcttgaagcttgaagcttgaagcttgaagct 618
QY 1155 gacaagaagctcttatactatgacacagcttgaagcttgaagcttgaagcttgaagct 1214
DB 619 gacaagaagctcttatactatgacacagcttgaagcttgaagcttgaagcttgaagct 678
QY 1215 gtcaaaatccattatagcagcctctgcttaagatcccccggttaatttcgaagaagat 1274
DB 679 gtcaaaatccattatagcagcctctgcttaagatcccccggttaatttcgaagaagat 738
DB 1275 tactcagagctgmaaaataccacacagcttgcgcaaaactctgctggaacaaatccatt 1334
DB 739 tactcagagctgmaaaataccacacagcttgcgcaaaactctgctggaacaaatccatt 798
QY 1335 tggagagagatattgaattgcaacacagctgctggttcttcaatgtgaattgacaa 1394
DB 799 tggagagagatattgaattgcaacacagctgctggttcttcaatgtgaattgacaa 858
QY 1395 gccaagt-gagcattgcaatgagcttgcacgcttgccttgccttgccttgccttgcct 1449
DB 859 gccaagt-gagcattgcaatgagcttgcacgcttgccttgccttgccttgccttgcct 918
QY 1450 agtg-tcaccttgcaagctgtg 1471
DB 919 agtg-tcaccttgcaagctgtg 941

```

```

RESULT 4
US-09-760-485-323
; Sequence 323, Application US/09760485
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0217
; CURRENT APPLICATION NUMBER: US/09/760,485
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1477

```

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 323
; LENGTH: 950
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (42)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (48)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (815)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (840)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (889)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-760-485-323

```

```

Query Match          39.7%; Score 615.6; DB 5; Length 950;
Best Local Similarity 96.2%; Pred. No. 3,8e-141;
Matches 657; Conservative 4; Mismatches 16; Indels 6; Gaps 3;

```

```

QY 795 atggcattgaaggtctggacaagatagaagatgaagaatcttcataagatttgcatt 854
DB 259 atcttcattgaaggtctggacaagatagaagatgaagaatcttcataagatttgcatt 318
DB 855 tctcgaagaacgtctgaagatgacacacaggaagaatcttcataagatttgcatt 914
DB 319 tcatgaaaacgatacagagatgacacacaggaagaatcttcataagatttgcatt 378
QY 915 aggaagatcaaaagcagcttgaagctcttggaagataataatgataaacaagaagaga 974
DB 379 aggaagatcaaaagcagcttgaagctcttggaagataataatgataaacaagaagaga 438
QY 975 cgaagaagaagaacagcttgaagatgacacacaggaagaatcttcataagatttgcatt 1034
DB 439 cgaagaagaagaacagcttgaagatgacacacaggaagaatcttcataagatttgcatt 498
QY 1035 atgtcataagttgagcagcagatgaagaacacatctgttatacagtgagctgaagaagat 1094
DB 499 atgtcataagttgagcagcagatgaagaacacatctgttatacagtgagctgaagaagat 558
QY 1095 actacacacatgagcagcagcttgaagcttgaagcttgaagcttgaagcttgaagct 1154
DB 559 actacacacatgagcagcagcttgaagcttgaagcttgaagcttgaagcttgaagct 618
QY 1155 gacaagaagctcttatactatgacacagcttgaagcttgaagcttgaagcttgaagct 1214
DB 619 gacaagaagctcttatactatgacacagcttgaagcttgaagcttgaagcttgaagct 678
QY 1215 gtcaaaatccattatagcagcctctgcttaagatcccccggttaatttcgaagaagat 1274
DB 679 gtcaaaatccattatagcagcctctgcttaagatcccccggttaatttcgaagaagat 738
QY 1275 tactcagagctgmaaaataccacacagcttgcgcaaaactctgctggaacaaatccatt 1334
DB 739 tactcagagctgmaaaataccacacagcttgcgcaaaactctgctggaacaaatccatt 798
QY 1335 tggagagagatattgaattgcaacacagctgctggttcttcaatgtgaattgacaa 1394
DB 799 tggagagagatattgaattgcaacacagctgctggttcttcaatgtgaattgacaa 858
QY 1395 gccaagt-gagcattgcaatgagcttgcacgcttgccttgccttgccttgccttgcct 1449
DB 859 gccaagt-gagcattgcaatgagcttgcacgcttgccttgccttgccttgccttgcct 918
QY 1450 agtg-tcaccttgcaagctgtg 1471

```





```

RESULT 11
US-09-808-383-5037
; Sequence 5037, Application US/09808383
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: 1600,1046-002
; CURRENT APPLICATION NUMBER: US/09/808,383
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 09/397,022
; PRIOR FILING DATE: 1999-09-15

```



	Accession	Index	Gaps
QY	170 cctctgctctgtagcagcggaatggagaaagatccacagggctggaagagctgtagtccaggt	229	
Db	1285 ccttggaatgaaagggagaaacagatccctacaaaggcggaagccctgaaagttcctcaagg	1344	
QY	230 ttgcacaggaactatggggtctcagaggtctgacagggccctcaggtccagtttgaccnaa	289	
Db	1345 caagaaagtgtaaaactcgggccccaggtccagttgctctcccaagttctctcttgacata	1404	
QY	290 ggaagaaagctgcgtcgtcgcggaacctggaaccaaaaggagaaagtgtgaataagtgacct	349	
Db	1405 ggaacatgtagtaactccgtgtcccaaaaggccaacagggctctccgtgtacctctgtctc	1464	
QY	350 ccagagactccaagtattctccgtgtccagctcggaagaagaggtccctcttgggaacaggg	409	
Db	1465 cctgtgtacagcagggcctctcgatctccagggccctcagaggttagacatgtgtctcaagg	1524	
QY	410 aacatcagagctccaaaggaacacaggtcctaaaggagagagctcggaagcccaaggaaagta	469	
Db	1525 aacttcgggccttcgggtgtgaaccaaggtttcaaaaggaaagctcggaagcccaaggggaacca	1584	
QY	470 ggtgtctcttgcaatgcagagatctacaagggtcgaaaggtctccacaggtcccaagggaa	539	
Db	1585 ggagccacatggtattcagggctcgaatagggcccaagcccggtgaaagaggaanaaagggtccc	1644	
QY	530 aagagtgcccccctgtgtgcaagagagcccaagggaaatgtcttgagcagacagagacccggga	589	
Db	1645 agaaagttaacccaagaaacacttggctctccacagggccagctggaagaaaggtgtgctccgtgc	1704	
QY	590 ccgcgcggtccaaagagagctccagagttccacaggggccccaggaactcaagggggacaga	649	
Db	1705 aatcgtgttttcacaggtcctgatgtgttaacctggtgccaagaggtgtgtccaaggaagag	1764	
QY	650 ggtgtcctcttgaaacagagaaatcaaaagtgaaagcgggtctccacagacagtgtgt	704	
Db	1765 ggtcctgtaggtcttccaaagccaagaaagaaagccaaagcgggtatccagagactccag	1819	

Query Match	8.28;	Score 127.2;	DB 6;	Length 4748;
Best Local Similarity	52.4%;	Pred. No. 1.9e-21;		
Matches 279; Conservative	0;	Mismatches 255;	Indels 0;	Gaps 0;

[illegible]

```

OY      650 ggtgttctctggaagacagaagatcaaaagtcaaacgggtcttcacaacgtctg 704
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1765 ggctcctgtagttctcttcagaccaccaaggaaagcagcgaggatccaggactcag 1819
                                     ||| ||||| | | | | | | | | | | | |
RESULT  14
US-60-278-258-11304
: Sequence 11304, Application US/60278258
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Ial, preeti
: APPLICANT: diep, dinh
: TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
: TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
: FILE REFERENCE: GX-0010-1 p
: CURRENT APPLICATION NUMBER: US/60/278,258
: CURRENT FILING DATE: 2001-03-23
: NUMBER OF SEQ ID NOS: 17730
: SOFTWARE: PERL Program
: SEQ ID NO 11304
: LENGTH: 4748
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
NAME/KEY: misc_feature

```

```

RESULT 15
US-60-278-258-10582
; Sequence 10582, Application US/60278258
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; FILE REFERENCE: GX-0010-1 P
; CURRENT APPLICATION NUMBER: US/60/278,258
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 17730
; SOFTWARE: PERL Program
; SEQ ID NO 10582
; LENGTH: 4796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1099943.4
; NAME/KEY: unsure
; LOCATION: 3618, 3629, 3634, 3637, 4408
; OTHER INFORMATION: a, t, c, g, or other
US-60-278-258-10582

```



**THIS PAGE BLANK (USPTO)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2001, 02:59:11 ; Search time 2762.57 Seconds  
(without alignments)  
8689,715 Million cell updates/sec

Title: US-09-454-223-1

Perfect score: 1552  
Sequence: 1 gctagcgaaatccaccacga.....aggcactgtagaactgtaacc 1552

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Checked: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_ba1:\*
- 2: gb\_ba2:\*
- 3: gb\_ba3:\*
- 4: gb\_in1:\*
- 5: gb\_in2:\*
- 6: gb\_in3:\*
- 7: gb\_cm:\*
- 8: gb\_ov:\*
- 9: gb\_pat1:\*
- 10: gb\_pat2:\*
- 11: gb\_ph:\*
- 12: gb\_pl1:\*
- 13: gb\_pl2:\*
- 14: gb\_pl3:\*
- 15: gb\_pl4:\*
- 16: em\_ba1:\*
- 17: em\_ba2:\*
- 18: em\_fun:\*
- 19: em\_htgo\_hum:\*
- 20: em\_htgo\_inv:\*
- 21: em\_htgo\_rod:\*
- 22: em\_htg\_hum1:\*
- 23: em\_htg\_hum2:\*
- 24: em\_htg\_hum3:\*
- 25: em\_htg\_hum4:\*
- 26: em\_htg\_hum5:\*
- 27: em\_htg\_hum6:\*
- 28: em\_htg\_hum7:\*
- 29: em\_htg\_hum8:\*
- 30: em\_htg\_inv1:\*
- 31: em\_htg\_inv2:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_rod:\*
- 34: em\_hum1:\*
- 35: em\_hum2:\*
- 36: em\_hum3:\*
- 37: em\_hum4:\*
- 38: em\_hum5:\*
- 39: em\_hum6:\*
- 40: em\_hum7:\*
- 41: em\_in:\*
- 42: em\_cm:\*
- 43: em\_or:\*

44: em\_ov:\*

45: em\_pat:\*

46: em\_ph:\*

47: em\_pl:\*

48: em\_ro:\*

49: em\_sts:\*

50: em\_sy:\*

51: em\_un:\*

52: em\_vl:\*

53: gb\_sts1:\*

54: gb\_sts2:\*

55: gb\_sts3:\*

56: gb\_sy:\*

57: gb\_un:\*

58: gb\_vl1:\*

59: gb\_vl2:\*

60: gb\_hc91:\*

61: gb\_hc92:\*

62: gb\_hc93:\*

63: gb\_hc94:\*

64: gb\_hc95:\*

65: gb\_hc96:\*

66: gb\_hc97:\*

67: gb\_hc98:\*

68: gb\_hc99:\*

69: gb\_hc10:\*

70: gb\_hc11:\*

71: gb\_hc12:\*

72: gb\_hc13:\*

73: gb\_hc14:\*

74: gb\_hc15:\*

75: gb\_hc16:\*

76: gb\_hc17:\*

77: gb\_hc18:\*

78: gb\_hc19:\*

79: gb\_hc20:\*

80: gb\_hc21:\*

81: gb\_hc22:\*

82: gb\_hc23:\*

83: gb\_hc24:\*

84: gb\_hc25:\*

85: gb\_pr1:\*

86: gb\_pr2:\*

87: gb\_pr3:\*

88: gb\_pr4:\*

89: gb\_pr5:\*

90: gb\_pr6:\*

91: gb\_pr7:\*

92: gb\_pr8:\*

93: gb\_pr9:\*

94: gb\_ro1:\*

95: gb\_ro2:\*

96: gb\_in4:\*

97: gb\_pr10:\*

98: em\_ba3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	790.4	50.9	1183	94 BC003705	BC003705 Mus muscu
2	778.6	50.2	1253	94 M05SPD	L40156 Mus musculu
3	720.2	46.4	879	10 AX090039	AX090039 Sequence
4	720.2	46.4	879	93 HSGP39MR	Z15017 H.sapiens m
5	710	45.7	1803	93 HSCD40	X67878 H.sapiens m
6	710	45.7	1816	97 HUMCD40L	L07414 Human CD40-
7	705.2	45.4	1822	93 HSTRAPA	X68550 H.sapiens T
8	698.8	45.0	1058	89 AF344841	AF344841 Cercocobu



Db	549	GAGCCCGAAGGGAATCTGTGCACAGCAGGACTCTGCCGACCTGCCGTCACACAGSAGCTC	608
Oy	612	caggttcctcaggaggcccccaagaactcctaaaggaggagagagtgttctctggaacagaggaa	671
Db	609	CAGGTTCCAGGAGGGCCCCCAGCAGACTCAAGAGGGGACAGAGTGTCTCGAGACAAGAA	668
Oy	672	tcaaagtgtgaaaaggaggtctccagacagtgctgcctctgaagcagcagatgttaggccttaa	731
Db	669	TCAAAGCTGAAAAGGGGGCTTCCACACACTGCTGCTTAGCAGCAGCATGTGAGGCTTA	728
Oy	732	aaggaaabactaacagcgctctagagglttgctctctcccatatcagaaagctcatgtttcc	791
Db	729	AAGGAAAACTCACGCGTTAGAGGTTGCTTCTCCCACTATCAGAAAGCTGCATTGTTC	788
Oy	792	ctgatggccatalagaaaglttgacaagat	819
Db	789	CTGATGCGCCCAAGTGCTTGACAGACAAGAT	816
RESULT	2		
MUSSPD			
LOCUS			
DEFINITION	MUS musculus (clones 12.1, 2.1 and 4.1) surfactant protein D (sfldp) mRNA, complete cds.	ROD	12-MAR-1996
ACCESSION	L40156.1	GI:	1129061
VERSION			
KEYWORDS	C-type lectin; collagenous lectin; collectin; surfactant protein D.		
SOURCE	Mus musculus (strain B6/CBAFJ) cDNA to mRNA.		
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1253) Motwani,M., White,R.A., Guo,N., Dowler,L.T., Tauber,A.I. and Sastry,K.N.		
REFERENCE			
AUTHORS			
TITLE	Mouse surfactant protein-D. cDNA cloning, characterization, and gene localization to chromosome 14		
JOURNAL	J. Immunol. 155 (12), 5671-5677 (1995)		
MEDLINE	96094460		
FEATURES			
SOURCE	Location/Qualifiers		
	1..1253		
	/organism="Mus musculus"		
	/strain="B6/CBAFJ"		
	/db_xref="taxon:10090"		
	/clone="12.1; 2.1; 4.1"		
	/sex="female"		
	/dev_stage="6-8 weeks"		
	/tissue_type="lung"		
	/clone_1lp="lambda zap II library from stratagene"		
	/chromosome="14"		
mRNA	1..1253		
5'UTR	1..5		
CDS	6..1130		
	/gene="Sfcp4"		
	/note="Sp-D"		
	/codon_start=1		
	/product="surfactant protein D"		
	/protein_id="AAA92021.1"		
	/db_xref="GI:1129062"		
	/translation="MLPFLSMIVLLVPLGLNIGAEKMSLSQSVPTNTCTLVMSPTENCLORORDDRDRREGRCRKCKDPGLDPNGLSLQGPPTPVGHKGNGSAGEPRGEGRLSGPGGLPIGIPAPGKEGPSKKQGNITPOGPPCKGRGAPRGEGVAGMGOSTAKSSSTGPEGERGAVGVQAPCNAGAAGPAGPAGPGAPSGPDLKGDGVPGDRIJKGSSEKPSALROOMALKRLORLEVAFFSHYKAALFPQRSYGDKIFPADESKPEDMAOEMKGOALGOLASPRSATENAAIIOOLLTHANKAAF.LMTDVGTEGKFTYPGEPLVYSNMADGEPNNNGAACVEIFTNGMDNRKACEQRVLICPF"		
s1g_peptide	6..62		
	/gene="Sfcp4"		
gene	6..1130		
	/gene="Sfcp4"		
mat_peptide	63..1127		
	/gene="Sfcp4"		
	/product="surfactant protein D"		

[illegible]



QY 1035 atgtcataagtgaggccagcagtaaaacaacatctgtgttaccagtggtcgaaagaagat 1094  
 |||  
 DB 395 ATGTCAATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGGCTGAAAGAGAT 454  
 QY 1095 actacaccatgaacaacaactctgttaacctgggaaatggaaacagctgacccttaaa 1154  
 |||  
 DB 455 ACTACACCATGACCAACACTTGGTAACCTGGAAATGGAAACAGCTGACCGTTAAAA 514  
 QY 1155 gacaaagactatataatcatatgcacaaagtcacactctgttccaaatcggaactcg 1214  
 |||  
 DB 515 GACAAAGACTAT 574  
 QY 1215 gccaagctcatattatagcagcctctgcttaaaagtcaccccggttaattcggagaatct 1274  
 |||  
 DB 575 GTCAACCTCATATTATATAGCAGCCTGCTTAAGTCCCGGTAGATTCGAGAAATCT 634  
 QY 1275 tactcagagctgcgaatatacacaagcttcgcgaacactctgcgggcaacaatccatcact 1334  
 |||  
 DB 635 TACTCAGAGCTGCAATATACCAACAGTTCGCCCAACCTTGGGGCAACATCATTCAC 694  
 QY 1335 tggagagagbalttgaattgcacaacagctgctcggttcttgcacatgtaactgacaa 1394  
 |||  
 DB 695 TGCGAGAGATATTGTAATGCAACACAGTGTCTGCTGTTTGTCAATGTGACTGATCAA 754  
 QY 1395 gccaagtgccaagtcagcactgctcagctccttgccttaccacaactctgaaacagctg 1454  
 |||  
 DB 755 GCCAAGTGAAGCTGACCTGACCTGCTTGTGCTTACTCAACCTGTAACAGTGT 814  
 QY 1455 caactgcagagctgtgtgagctgcagctgcgtgagagcttcataatacagacaggtctaa 1514  
 |||  
 DB 815 CACCTTGCAGAGCTGTGTGTGAGCTGACCTGAGAGTCTTATATATACACAGCGCTTAA 874  
 QY 1515 gccca 1519  
 |||  
 DB 875 GCCCA 879

## RESULT 5

HSCD40 1803 bp mRNA PRI 06-JUN-1997  
 LOCUS H.sapiens mRNA for CD40 ligand.  
 DEFINITION X67878 S50586  
 VERSION X67878.1 GI:38411  
 KEYWORDS glycoprotein.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota: Metazoa: Chordata: Granata: Vertebrata: Euteleostomi:  
 Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.  
 1 (bases 1 to 1803)

REFERENCE 1  
 AUTHORS Spriggs, M.  
 TITLE Direct Submision  
 JOURNAL Submitted (28-JUN-1992) M. Spriggs, Immunex Res & Development  
 CORPORATION, 51 University Street, Seattle WA 98101, USA  
 2 (bases 1 to 1803)  
 AUTHORS Spriggs, M.K., Arncliffe, R.J., Strockbine, L., Clifford, K.N.,  
 Macduffy, B.M., Sato, T.A., Maliszewski, C.R. and Fanslow, W.C.  
 REFINANCE Recombinant human CD40 ligand stimulates B cell proliferation and  
 immunoglobulin E secretion  
 JOURNAL J. Exp. Med. 176 (6), 1543-1550 (1992)  
 MEDLINE 93094757  
 FEATURES Location/Qualifiers  
 source 1..1803  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /cell\_type="peripheral blood T-cell"  
 46..831  
 /codon\_start=1  
 /product="CD40 ligand"  
 /protein\_id="CAA48077.1"  
 /db\_xref="GI:38412"  
 /db\_xref="SWISS-PROT:P29965"  
 /translation="MIETYNQSPRSAAAGLPISMKIFWLLTFLITOMIGSALFAV  
 YLHRLDKIEDERNLHEDFVFMKTIQRCRTGRSLNLNCEIRKQSFBEFVDIMLNK"

## CDS

1..1803  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /cell\_type="peripheral blood T-cell"  
 46..831  
 /codon\_start=1  
 /product="CD40 ligand"  
 /protein\_id="CAA48077.1"  
 /db\_xref="GI:38412"  
 /db\_xref="SWISS-PROT:P29965"  
 /translation="MIETYNQSPRSAAAGLPISMKIFWLLTFLITOMIGSALFAV  
 YLHRLDKIEDERNLHEDFVFMKTIQRCRTGRSLNLNCEIRKQSFBEFVDIMLNK"

ESTKRESEKNOGDONPOIAHVISEASSKTSVLQAEKGYTMMNLVTLENGKO  
 LTVKQGLYITTAQVTFPCSNRPAASDAPFASLCLKSPREIRILLRAANTHSSAKPC  
 GQOSIHLGSEFELQPGASVFNVTPOVSHTGTFTSFLLKL"  
 112..183  
 /note="CD40 ligand"  
 /product="NH2 signal /anchor"  
 BASE COUNT 510 a 456 c 344 g 493 t  
 ORIGIN

Query Match 45.7%; Score 710; DB 93; Length 1803;  
 Best Local Similarity 98.6%; Pred. No. 9, 6e-171;  
 Matches 716; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 795 atggcagatgaaggttgagacagatagaagaatgaagaactcttcataagattctgcat 854  
 |||  
 DB 179 ATCTTATGAAAGTTGGACCAAGATGAAAGATGAAAGATCTTCAATGAAATTTGTAT 238  
 QY 855 tcatgaaacgatagagagatgacaacagggagaagaatcttacttactgaactgtg 914  
 |||  
 DB 239 TCATGAAACGATACAGAGATGCACACAGAGAGAGATCTTATCTTACTGAACTGTG 298  
 QY 915 agagattaaaagccagcttgaaagcttgagagataataatgtaaaacaaagagaga 974  
 |||  
 DB 299 AGGAGATTAAACCCAGTTTGAAGCTTTGTGAAGATATATATATATATATATATAT 358  
 QY 975 cgaagaagaagaacagcttgaaatgcaaaaagggtgatacagaatctcaaatctgggac 1034  
 |||  
 DB 359 CGAAGAAACGAAACACCTTGAATGCAAAAAGGTATGAAATCTTCAATGCGGAC 418  
 QY 1035 atgtcataagtgaggccagcagtaaaacaacatctgtgttaccagtggtcgaaagaagat 1094  
 |||  
 DB 419 ATGTCAATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGGCTGAAAGAGAT 478  
 QY 1095 actacaccatgaacaacaactctgttaacctgggaaatggaaacagctgacccttaaa 1154  
 |||  
 DB 479 ACTACACCATGACCAACACTTGGTAACCTGGAAATGGAAACAGCTGACCGTTAAAA 538  
 QY 1155 gacaagaactatataatcatatgcacaaagtcacactctgttccaaatcggaactcg 1214  
 |||  
 DB 539 GACAAAGACTCTAT 598  
 QY 1215 gccaagctcatattatagcagcctctgcttaaaagtcaccccggttaattcggagaatct 1274  
 |||  
 DB 599 GTCAACCTCATATTATATAGCAGCCTGCTTAAAGTCCCGGTAGATTCGAGAAATCT 658  
 QY 1275 tactcagagctgcgaatatacacaagcttcgcgaacactctgcgggcaacaatccatcact 1334  
 |||  
 DB 659 TACTCAGAGCTGCAATATACCAACAGTTCGCCCAACCTTGGGGCAACATCATTCAC 718  
 QY 1335 tggagagagbalttgaattgcacaacagctgctcggttcttgcacatgtaactgacaa 1394  
 |||  
 DB 719 TGCGAGAGATATTGTAATGCAACACAGTGTCTGCTGTTTGTCAATGTGACTGATCAA 778  
 QY 1395 gccaagtgccaagtcagcactgctcagctccttgccttaccacaactctgaaacagctg 1454  
 |||  
 DB 779 GCCAAGTGAAGCTGACCTGACCTGCTTGTGCTTACTCAACCTGTAACAGTGT 838  
 QY 1455 caactgcagagctgtgtgagctgcagctgcgtgagagcttcataatacagacaggtctaa 1514  
 |||  
 DB 839 CACCTTGCAGAGCTGTGTGTGAGCTGACCTGAGAGTCTTATATATACAGCAGCGGTTA 898  
 QY 1515 gccca 1520  
 |||  
 DB 899 AGCCCA 904

RESULT 6  
 HUMCD40L 1816 bp mRNA PRI 27-APR-1993  
 LOCUS HUMCD40L  
 DEFINITION Human CD40-ligand mRNA, complete cds.  
 ACCESSION L07414  
 VERSION L07414.1 GI:180123

KEYWORDS CD4/CD8-associated protein; CD40-ligand.  
 SOURCE Homo sapiens (library: lambda gtl10) cDNA to mRNA.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1816)  
 Gauchat, J., F.M., Aubry, J., P., Mazzei, G.J., Lile, P., Jomotte, T.,  
 Elson, G., and Bonnefoy, J.-Y.,  
 Human CD40-ligand: Molecular cloning, cellular distribution and  
 regulation of expression by factors controlling IgE production  
 FEBS Lett. 315, 259-266 (1992)  
 MEDLINE 91138085  
 JOURNAL  
 FEATURES  
 SOURCE

Location/Qualifiers  
 1..1816  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /cell\_type="T-Lymphocyte"  
 /tissue="liver"  
 /lambda gtl10"  
 40..825  
 /note="hydrophobic region (bps. 76..171): extracellular  
 domain (bps. 172..822); glycosylation sites (bps. 55..63  
 and 757..765)."  
 /codon\_start=1  
 /product="CD40 surface protein"  
 /protein\_id="AA35662.1"  
 /db\_xref="GI:180124"  
 /translation="MIEETNOTSPRSATGLPISMKIFMYLTVFLITOMIGSALFAY  
 YLHRLDKIEDERLHEDFVFMKTIOCNTERSLNCEETKSQEGFVKDINMK  
 EETKRENSFEQKDONPOIAAHVISEASSTKTSVLOMAKEGYTMSNNLYTENKQ  
 LTVRQGLYLYIAQVTFCSNREASQAPFIASICLSKSPGRPRILLRAANTHSSAKPC  
 GQOSIHGQVFEIOPGASVFNVTDPQSVSHGTFISRLKL"  
 1518..1581  
 /note="dinucleotide (CA) repeat"  
 /rpt\_unit="1518..1519 492 t  
 repeat\_region

BASE COUNT 520 a 461 c 343 g 492 t  
 ORIGIN

Query Match 45.7%; Score 710; DB 97; Length 1816;  
 Best Local Similarity 98.6%; Pred. No. 9, 6e-171;  
 Matches 716; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 795 atggccatagaggttgagagatgaagaagaagaattctcagaagatttgat 854  
 |||  
 DB 173 ATCTTCATAGAGAGTTGGACACAGATGAGATGAAGAGATCTTCATGAAGATTGCTAT 232  
 QY 855 tcatgaaacagatcagagatgcacacagaagaagaatccttactactgaactgtg 914  
 |||  
 DB 233 TCATGAAACGATACAGATGCAACACAGAGAGAGATCCTTATCTTACTGAACTGTG 292  
 QY 915 agagagataaagccagttgagaggttgagagatataatgtaacaagaagaga 974  
 |||  
 DB 293 AGGAGATTAAACCGATTGGAAGGCTTTGTGAGAGATTAATGTTAAACAAAGAGAGA 352  
 QY 975 cgaagaaagaagaacagcttgaaatgcacaaaggatcagaatcctcaaatgtggcac 1034  
 |||  
 DB 353 CGAAGAAAGAAAACACTTTGAATGCAAAAAGTGATGAGATCTCAAAATGGCGCAC 412  
 QY 1035 atgtcataagtgagcagcagtaaaacacatctgttaccatggagcgcgaagaagat 1094  
 |||  
 DB 413 ATGTCAVTAAGTGAGCGCACACTTAAACACATCTGTGTACAGGCGCTGAAAAAGGAT 472  
 QY 1095 actacacatgagcaacaactgtgtacacctggaaatgcgaagaagaagctgacgttaaa 1154  
 |||  
 DB 473 ACTACACCTVAGCAACAACCTTGTAACCTGGAAATGGGAACAGCTGACCGTTAAA 532  
 QY 1155 gacaaagacatcattatctatagcgaagacacccctgttccaatcgggaagctcga 1214  
 |||  
 DB 533 GACAAAGACTCATATATATCTATGACCAAGTACCTCTGTCCAAATCGGGAAGCTTGA 592  
 QY 1215 gtcaagctccatattatagcagcagctgtgactaaagtcgccggtatgtaagaatct 1274  
 |||  
 DB 593 GTCAAGCTCATATATATGACCAAGCTGTGCTAAAGTCCCGCGGTAGATTGAGAGATCT 652

QY 1275 tactaagagctgcaaatatccacagcttcgccaaacttcgagcaacaatccatcact 1334  
 |||  
 DB 653 TACTCAGAGCTGCAAAATATCCACAGATTCGCCCAAACTTCGGGCAACATCCATTCACCT 712  
 QY 1335 tggagagagatcttggaattgcacaagaagctgctgtgtgtgtcgaatgtaactgacaa 1394  
 |||  
 DB 713 TGGAGAGAGATTTGAAATGCAACAGAGTCTTCGGGTGTTCATATGATGATGATCCAA 772  
 QY 1395 gccaaagtgcacatgacagctgcttcacgctccttgcttaccacaaactgcgaagtg 1454  
 |||  
 DB 773 GCCAAGTAGAGCATGACATGCGCTTACGCTTGTGCTTACTCAAACTGTGAACAGTGT 832  
 QY 1455 cacttcagagcgtgtgtgagctgacgctgagagcttcataatcagacagcttaa 1514  
 |||  
 DB 833 CACCTTCAGAGCTGTGTGAGCTGACGCTGGAGTCTTCAATATACAGCAGCGGTTA 892  
 QY 1515 gcccaa 1520  
 |||  
 DB 893 AGCCCA 898

RESULT 7  
 HSTRAPA  
 LOCUS HSTRAPA 1822 bp mRNA PRI 30-JUN-1993  
 DEFINITION H.sapiens TRAP mRNA for ligand of CD40.  
 ACCESSION X68550.1  
 VERSION X68550.1 GI:37269  
 KEYWORDS T-cell activation; TNF related; transmembrane protein; TRAP gene.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1822)  
 Graf, D., Korthauer, U., Mages, H.W., Senger, G., and Kroczeck, R.A.  
 Cloning of TRAP, a ligand for CD40 on human T cells  
 Eur. J. Immunol. 22 (12), 3191-3194 (1992)  
 JOURNAL 93076854  
 MEDLINE  
 FEATURES  
 SOURCE

1..1822  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="X"  
 /tissue\_type="peripheral blood"  
 /cell\_type="T-Lymphocyte"  
 /map="Xq26.3 - Xq27.1"  
 57..842  
 /gene="TRAP"  
 57..842  
 /note="CD40 ligand"  
 /codon\_start=1  
 /protein\_id="CAA48554.1"  
 /db\_xref="GI:37270"  
 /db\_xref="SWISS-PROT:P29965"  
 /translation="MIEETNOTSPRSATGLPISMKIFMYLTVFLITOMIGSALFAY  
 YLHRLDKIEDERLHEDFVFMKTIOCNTERSLNCEETKSQEGFVKDINMK  
 EETKRENSFEQKDONPOIAAHVISEASSTKTSVLOMAKEGYTMSNNLYTENKQ  
 LTVRQGLYLYIAQVTFCSNREASQAPFIASICLSKSPGRPRILLRAANTHSSAKPC  
 GQOSIHGQVFEIOPGASVFNVTDPQSVSHGTFISRLKL"  
 186..839  
 /gene="TRAP"  
 186..839  
 /polya\_signal  
 1800..1805  
 /polya\_signal  
 1803..1808  
 BASE COUNT 516 a 465 c 346 g 495 t  
 ORIGIN

Query Match	45.4%	Score 705.2	DB 93	Length 1822
BosLC Local Similarity	98.2%	Pred. No. 1,66-169		
Matches 713	Conservative 0	Mismatches 13	Indels 0	Gaps
QY	795	atgagcatalaagaagctctgacacagaatagaagaatagaagaatctcatgaagatttctgat	854	
Db	190	ATCTTCATAGAGAGCTTGACACAGATTACAAAGTGAAGGAATCTTCATGAAGATTTTGTAT	249	
QY	855	tcatlgaataacgatacagaagatgcacaacagagaagaatccctatccctacatgcactgtg	914	
Db	250	TCATGAAAAACGATCATACAGATGCAACACAGAGAAAGATCTTATCTTACTGAACTGTG	309	
QY	915	agagagatttaaaagacagcttggtaagagctcttggtaagagataatgaatgaataaagaagaga	974	
Db	310	AGGAGATTAAAAAGCCAGCTTGAACGGCTTTGGAAAGGATTAATTAAGTTAAACAAAGAGAGA	369	
QY	975	cgaagaataaagaacacgctcttgaaatgcacaaagaatgaatcagaatccctcaatctgcgcac	1034	
Db	370	CGAAGAAAGAAACACGCTTGTAATGCAAAAAGTGATTCAGATTCCTCAATTTGGGGCAC	429	
QY	1035	atgtcataagtgaagccagcagataaacaacatctgtgttcacagtgggctgtaaaagat	1094	
Db	430	ATGTCAATAGTAGAGCCAGCCAGCAGTAAACAACTCTGTGTACAGTGGCGGTGAAAAAGAT	489	
QY	1095	actacacatgaagaacaaacttggtaaccccttgaaataatgggaacagctacacgttaaaa	1154	
Db	490	ACTACACCATATGACAACTTGTAACCTCGGAAATGGGAACACCTCACCGTTAAAA	549	
QY	1155	gacaaagacatcatatcatatctatgcacaaatcactctctgtctcacaatcgggaagcttga	1214	
Db	550	GACAAGGACTCTATTATATCTATCTGCCAAGTCACTCTGTCCAAATCGGGAAGCTTGA	609	
QY	1215	gtcaagctccatctatgatgcacagctctgctgttaagatcccccgttagatcttgagaagaatct	1274	
Db	610	GTCAAGCTCCATTTATATAGCCAGCCTCTGCTTAAAGTCCCGCGTGAATTTGGAAGAATCT	669	
QY	1275	tactcaagatctgcacaaataaccacacagctctgcgcacaaacctctgcggacacaaatcact	1334	
Db	670	TACTCAGAGCTGCAAATATACCCACAGTTCCGCCAAACCTTGCGGCAACATTCATTCACT	729	
QY	1335	tggaagaagatctcttgaatttgcacacaaagatgctcgtgtgttgcataatgtaagctgata	1394	
Db	730	TGGAGAGCGATTTTGAATTTGCAACACAGGCTCTTCGAGTTTGTCAATGATCAGTATCCAA	789	
QY	1395	gcacaagtgaagcatalgcagacatgcagctctgcacgtctctgtgcttactcaaaactctgaacag	1454	
Db	790	GCCAACTGACGATGCGCATGCGTCTTACAGTCTCTTGGCTTACTCAAACTGTGAACACTGT	849	
QY	1455	caactctgcacagctgtgtgttgcagctgcagctctgcagctctcacaatacagcacagcttcaa	1514	
Db	850	CACCTTCACAGCTGTGTGTGACGACGACGCTGGAGCTTCTCATATACAGACACAGCGGTTA	909	
QY	1515	gcacca 1520		
Db	910	AGCCCA 915		
RESULT	8			
AF344841	1058 bp	mRNA	PRI	17-APR-2001
LOCUS				
DEFINITION	Cercopithecus torquatus atys CD154 protein mRNA, complete cds.			
ACCESSION	AF344841			
VERSION	AF344841.1	GI:13655468		
KEYWORDS				
SOURCE	sooty mangabey.			
ORGANISM	Cercopithecus torquatus atys			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eulipotyphla; Primates; Catarrhini; Cercopithecoidea;			
	Cercopithecidae; Cercopithecus.			
REFERENCE	1 (bases 1 to 1058)			
	Villinger, F., Bostik, P., Mayne, A.E., King, C.L., Genain, C.P.,			

[illegible]





```

/strain="Fisher 344"
/db_xref="taxon:10116"
/issue_type="jung"
26..1242
/gene="SP-D"
26..82
/partial
/gene="SP-D"
/feature="alternate start site"
26..1150
/gene="SP-D"
/codon_start=1
/product="primary translation product of SP-D"
/protein_id="AAA42170.1"
/db_xref="GI:207036"
/translation="MHFLSLVLYVLPGLDGAEMKTLISQSTINTCTLYLCSPTEN
GLPGKRCRGRGPRGKEDPGLPGMGLSGLPGRGVPKGEVSAEPKBERG
LVPGSPGPIISGPKRKGKGNIGPKGPKGEVAPKGEVAPKGEVAPKGEV
APKGEVAPKGEVAPKGEVAPKGEVAPKGEVAPKGEVAPKGEVAPKGEV
GLPDSALRQOMKLNKRLQLEAFAPSRKKAALPPDQSVGDKIFRANSEPEDE
KMKCRQAGQLASPRATENAVQILVTHASNAFLSMTDVTCEKFTTPTGEALYS
NMAPGSPNNNGAENCVELFTNGQNNKACGEORLVCEP"
44..82
/partial
/gene="SP-D"
/feature="alternate start site"
83..1147
/gene="SP-D"
/feature="putative"
/product="pulmonary surfactant protein SP-D"
1237..1242
/gene="SP-D"
/feature="putative"
BASE COUNT      318 a      313 c      402 g      232 t
ORIGIN
Query Match      45.0%; Score 697.8; DB 95; Length 1265;
Best Local Similarity 91.1%; Pred. No. 1.2e-167;
Matches 741; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 7 gaattccacacgaagcaatctgacatgctgcctctctccatgcttgccttctgt 66
    |||||
DB 1 GAATTCACACGAGAACCAATCTCCATGCTTCTCTCATGCTTCTCTCTGCTTGT 60
QY 67 acagccctctgggaatctctggagcagaatgaaagcctctgcagagatcagacc 126
    |||||
DB 61 ACAGCCCTCTGGCGATCTGGACCAAAATGAAGACCTTTCGACAGATCAATACAA 120
QY 127 caccctgacacctgtcatctgtatgcccacaaagaaatgagctgctgtctgtgagag 186
    |||||
DB 121 CACGTCACCCCTGATCTTGTGTAGTCCAAACAGAAATGGCTCTGCTGACGAGAC 180
QY 187 ggaaggagagagagctccacagagctgagaaagctgacagcttgcagagacctaag 246
    |||||
DB 181 GGAAGGAGAGAGAGCTCCACAGGCGGCGAAGAGGTGATCCAGGTTTCCAGACCTTATGGC 240
QY 247 gctctcaagagctgcaagggcctacagctcagcttgcacaaagagagaaatgagctctgc 306
    |||||
DB 241 ACTCTAGAGCTTCTCTGCGCCCTAGAGTCCAGTTGGGCGCAAGAGAGATGCTCTGC 300
QY 307 tggcgaacacctggacaaagagagaaagctgagactaaatgagacccctccagagacttccagat 366
    |||||
DB 301 TGGAGAACCTGGACAAAGGAGAACGCTGACCTAGTTGGACCTCCAGATCTCCAGATAT 360
QY 367 tccctgttccagctggagaaagagctccctctggagagcagagagaaacataagagctcagag 426
    |||||
DB 361 TTCTGGTCCGCGCTGGAAGAAAGCCCTCTGTGGAGCAAGGAAACATAGACATCCCAAGC 420
QY 427 caaacagagctcctaaagagagagctgggcccacaaagagaaatgagctcctctgagatgaa 486
    |||||
DB 421 CAATACAGGCTCTAAAGAGAGAGCTGGCGCGCAAGAGAGAGATAGTGTCTCCGCGATGCA 480

```

```

QY 487 aggatctacaggggcaaaagagctccacagagcccccagagagaaagagtgccccctgtgt 546
    |||||
DB 481 AGGATCTGCAAGGGGCAAAAGCCCTCTGCGCCCAAGGAAAGAGTGCCCTCTGTGA 540
QY 547 gcaagagagcccccagagaaatgcttgaagcagagagaccttgcagagcttgcagagagag 606
    |||||
DB 541 GCAAGAGAGCCCTTGGAATAGTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 607 agtccagagcttccagaggggccccagagactcaagggagagagagagtgcttccctggagagc 666
    |||||
DB 601 AGCTCCAGGTTCCAGGGGCGCTCCAGAGACTCAAGGGGAGAGAGAGAGAGAGAGAGAGAG 660
QY 667 aggaatcaaaagtgtaaaagcggcttccagacagtgctgtcctgagcagagatgagagc 726
    |||||
DB 661 AGGATATCAAAAGGCAAAAGTGACACTTCCAGACAGTCTGCTCTAGGACAGATGAGAGC 720
QY 727 cltaaaaggaanaactacacagctctagaggttgccttctccacatcagaagagctgcat 786
    |||||
DB 721 TTGGAATGGAAGAACTTACAGGCTCTAGAGGCTGCTTTTCTCGCTATAGAAAGCCGCGT 780
QY 787 gtccctgtatggccatagaaagcttgagacagat 819
    |||||
DB 781 CTTCCTGATGAGCCAAAGTGTGGAAGACAAAT 813
RESULT 11
AR044779      840 bp      DNA      PAT      29-SEP-1999
LOCUS      AR044779      Sequence 3 from patent US 5817516.
DEFINITION      AR044779
ACCESSION      AR044779
VERSION      AR044779.1 GI:5966244
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 840)
AUTHORS      Kehry, M. and Castle, B.
TITLES      Methods for proliferating and differentiating B cells with high
JOURNAL      density membrane CD40 ligand
FEATURES      Patent: US 5817516-A 3 06-OCT-1998;
            Location/Qualifiers
            source      1..840
            /organism="unknown"
BASE COUNT      263 a      182 c      181 g      214 t
ORIGIN
Query Match      43.9%; Score 681.2; DB 9; Length 840;
Best Local Similarity 99.6%; Pred. No. 2.1e-163;
Matches 683; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 795 atggcacaagagagcttgacacagatagaaatgaaagaaatcttcaatgaagatttgtat 854
    |||||
DB 155 ATCTTCATAGAAAGTTGACAAAGATAGAAAGATGAAAGAAATCTTCAATGAAATTTGTAT 214
QY 855 tcatgaaacagatagagatgtaacacacagagaaagatcttctatcttctaaactgtg 914
    |||||
DB 215 TCATGAAAGATACAGAGATGCAACACAGAGAGAAAGATCTTATCTTACGAACTGTG 274
QY 915 aggaagctaaagcagcttgaagagcttctgaaagataatgattcaaaacaaagagagaga 974
    |||||
DB 275 AGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATATATGTTAAACAAAGAGAGAG 334
QY 975 cgaagaagaaacacagcttgaaatgcaaaaagtgatcagaatcctcaaatctggagac 1034
    |||||
DB 335 CGAAGAAAGAAACAGCTTGAATATCAAAAGGATATGATCAATCTCAAAATGCGCGCAC 394
QY 1035 atgtcatagttgagcagcagcagtaaaacaaacatctgttaacagtgaggctgaaagagac 1094
    |||||
DB 395 ATGTCAATAGTGAAGCCAGAGTAAACAAACATCTGTGTACAGTGGCTGAAAGAGAT 454
QY 1095 actacacacatgagcaaacactgttaacccctgtaaaatggaagacagctgagccgttaaaa 1154
    |||||

```

RESULT	12
LOCUS	123893
DEFINITION	123893 840 bp DNA
ACCESSION	Sequence 1 from patent US 5540926.
VERSION	123893
KEYWORDS	GI:1603763
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 840)
TITLE	Aruffo, A., Hollenbaugh, D. and Ledbetter, J.A.
JOURNAL	Soluble and its use in B cell stimulation
FEATURES	Patent: US 5540926-A 1 30-JUL-1996;
source	Location/Qualifiers 1..840 +/organism="unknown"
BASE COUNT	263 a 182 c 214 t
ORIGIN	181 g

705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582

QY	155	ATCTTCATAGAAAGGCTTGACAAAGATAGACATGAAAGAAATCTTCATGAAAGATTTGGTAT	214
Db	155	ATCTTCATAGAAAGGCTTGACAAAGATAGACATGAAAGAAATCTTCATGAAAGATTTGGTAT	854
QY	855	tcacgaaacgatcaagagatgcacaacagagaagaatcctataccttaactgaactgtg	914
Db	215	TCATGAACCATACAGAGATGCACACAGAGAAAGATCCTTATCCTTACCTTACGAACTG	274
QY	915	aggagatlaaaagccagctttgaaagccttctgaaagatataatgtaaaacaagaagsga	974
Db	215	AGGAGATTTAAAAAGCCACTTTGAAGGCTTTGTGAAGATTTAATGTTAAAAAAGGAGGA	334
QY	975	Cgaagaagaanaacagctttgaaatgcaaaaagtgatcagaatcctcaaatcttgsgac	1034
Db	335	CGAAGAAGAAAAACGCTTTGAAATATCAAAAAGGTCATCGAATCCTCAATTTGGCGAC	394
QY	1035	atgtcatalaagtgsagccagcagatlaaacaacatctgtgttaagtgagcctbtaaaagat	1094
Db	395	ATGTCAATAAATGAGCCACAGCATGTAACAAACATCTGTGTTCACGTGGGCTTAAAAAAGAT	454
QY	1095	actacacgatgagcaacaacttgytlaaccttgaaatctgggaaacagctgtgacccctlaaa	1154

RESULT	13	
LOCUS	HACD40L	
DEFINITION	H.sapiens mRNA for CD40-ligand.	PRI
VERSION	X96710.1	13-FEB-1997
KEYWORDS	X96710.1 GI:1255924	
SOURCE	CD40-ligand.	
ORGANISM	human.	
REFERENCE	Homo sapiens	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 859)	
TITLE	Gramer, A.C., Bergman, M.C., Miura, Y., Fujita, K., Davis, L.S. and Lipsky, P.E.	
JOURNAL	The CD40 ligand expressed by human B cells costimulates B cell responses	
MEDLINE	J. Immunol. 154 (10), 4996-5010 (1995)	
REFERENCE	95248064	
AUTHORS	2 (bases 1 to 839)	
TITLE	Gramer, A.C.	
JOURNAL	Direct Submission	
	Submitted (27-JAN-1996) A.C. Gramer, UNSW Medical Center at Dallas, 5323 Harry Hines Blvd., Dept. of Rheumatology, Dallas, TX 75235-8577, USA	

```
FEATURES
source      Location/Qualifiers
1..639
```

```

/organism="Homo sapiens"
/isolate="patient B.S."
/db_xref="taxon:9606"
/chromosome="Xq25"
/dev_stage="3 years old"
/cell_type="B#T"
/cell_line="H1GMXL AO-EBV B#"
/clone="1"
/clone="9"
<1. ->839
MRNA
/Product="CD40-ligand"
BASE COUNT      264 a      181 c      180 g      214 t
ORIGIN

```

Query Match	42.98;	Score 666;	DB 91;	Length 839;
Best Local Similarity	99.18;	Pred. No. 1,6e-159;		
Matches 680;	Conservative 0;	Mismatches 5;	Indels 1;	Gaps 1;





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2001, 04:42:23 ; Search time 145.09 Seconds  
(without alignments)  
6716.544 Million cell updates/sec

Title: US-09-454-223-1

Perfact score: 1552  
Sequence: 1 gctgcgaatccaccagga.....agcatttagactgtacc 1552

Scoring table: IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_0601:\*

- 1: /cgnl\_9/gcgdata/geneseq/geneseq/NA1980.DAT:\*
- 2: /cgnl\_9/gcgdata/geneseq/geneseq/NA1981.DAT:\*
- 3: /cgnl\_9/gcgdata/geneseq/geneseq/NA1982.DAT:\*
- 4: /cgnl\_9/gcgdata/geneseq/geneseq/NA1983.DAT:\*
- 5: /cgnl\_9/gcgdata/geneseq/geneseq/NA1984.DAT:\*
- 6: /cgnl\_9/gcgdata/geneseq/geneseq/NA1985.DAT:\*
- 7: /cgnl\_9/gcgdata/geneseq/geneseq/NA1986.DAT:\*
- 8: /cgnl\_9/gcgdata/geneseq/geneseq/NA1987.DAT:\*
- 9: /cgnl\_9/gcgdata/geneseq/geneseq/NA1988.DAT:\*
- 10: /cgnl\_9/gcgdata/geneseq/geneseq/NA1989.DAT:\*
- 11: /cgnl\_9/gcgdata/geneseq/geneseq/NA1990.DAT:\*
- 12: /cgnl\_9/gcgdata/geneseq/geneseq/NA1991.DAT:\*
- 13: /cgnl\_9/gcgdata/geneseq/geneseq/NA1992.DAT:\*
- 14: /cgnl\_9/gcgdata/geneseq/geneseq/NA1993.DAT:\*
- 15: /cgnl\_9/gcgdata/geneseq/geneseq/NA1994.DAT:\*
- 16: /cgnl\_9/gcgdata/geneseq/geneseq/NA1995.DAT:\*
- 17: /cgnl\_9/gcgdata/geneseq/geneseq/NA1996.DAT:\*
- 18: /cgnl\_9/gcgdata/geneseq/geneseq/NA1997.DAT:\*
- 19: /cgnl\_9/gcgdata/geneseq/geneseq/NA1998.DAT:\*
- 20: /cgnl\_9/gcgdata/geneseq/geneseq/NA1999.DAT:\*
- 21: /cgnl\_9/gcgdata/geneseq/geneseq/NA2000.DAT:\*
- 22: /cgnl\_9/gcgdata/geneseq/geneseq/NA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	720.2	46.4	879	22	AAFS5539
2	710	45.7	1816	21	AAAS1745
3	681.2	43.9	840	16	AAAT05763
4	681.2	43.9	840	19	AAAV61063
5	679.6	43.8	840	15	AAOS7984
6	657.2	42.3	840	14	AAO41506
7	657.2	42.3	840	15	AAO67123
8	657.2	42.3	840	18	AAAT93782
9	654.2	42.2	840	20	AAZ27525
10	654.2	42.2	840	18	AAAT58122
11	652.4	42.0	840	16	AAO94091
					Human CD40-L CDNA.

12	648.2	41.8	786	15	AAO63959	Human CD40-L type
13	648.2	41.8	786	19	AAV38997	CD40 ligand gene u
14	648.2	41.8	786	19	AAV39000	Exemplary CD40 lig
15	648.2	41.8	786	19	AAV39002	Exemplary CD40 lig
16	648.2	41.8	786	19	AAV39003	Exemplary CD40 lig
17	648.2	41.8	786	19	AAV12852	CD40 ligand coding
18	638.6	41.1	1425	14	AAO41516	Human CD40-L/Fc fu
19	638.6	41.1	1425	20	AAZ27534	Human CD40-L/Fc fu
20	638.2	41.1	929	18	AAV58123	CDNA encoding yeas
21	638.2	41.1	929	20	AAZ27537	Human trimeric CD4
22	589	38.0	783	19	AAV42184	Exemplary nucleotl
23	563.6	36.3	864	19	AAV39004	CD40 ligand gene u
24	521.8	33.6	885	21	AAZ55541	Feline CD154 CDNA
25	520.2	33.5	885	21	AAZ55540	Feline CD154 CDNA
26	502.8	32.4	1878	21	AAZ55534	Canine CD154 CDNA
27	502.8	32.4	1878	21	AAZ55533	Canine CD154 CDNA
28	498	32.1	780	21	AAZ55542	Feline CD154 CDNA
29	498	32.1	780	21	AAZ55543	Feline CD154 CDNA
30	492.6	31.7	633	21	AAZ55544	Feline mature CD15
31	492.6	31.7	633	21	AAZ55545	Feline mature CD15
32	474	30.5	780	21	AAZ55536	Canine CD154 CDNA
33	474	30.5	780	21	AAZ55537	Canine CD154 CDNA
34	468	30.2	633	21	AAZ55538	Canine mature CD15
35	468	30.2	633	21	AAZ55539	Canine mature CD15
36	462.8	29.8	818	19	AAV61062	Murine CD40 ligand
37	456.2	29.4	783	15	AAO63960	Mouse CD40-L type
38	456.2	29.4	783	19	AAV12853	CD40 ligand coding
39	456.2	29.4	783	20	AAZ27524	Mouse CD40-L codin
40	456	29.4	606	19	AAV42183	Exemplary nucleotl
41	454.6	29.3	783	19	AAV38998	CD40 ligand gene u
42	454.6	29.3	783	19	AAV38999	Exemplary CD40 lig
43	454.6	29.3	783	19	AAV39001	Exemplary CD40 lig
44	453.6	29.2	782	14	AAO41507	Murine CD40-L DNA
45	447.6	28.8	878	20	AAZ27538	Mouse trimeric CD4

#### ALIGNMENTS

RESULT 1	
ID	AAFS5539 standard; DNA: 879 BP.
XX	
AC	AAFS5539;
XX	
DT	29-MAY-2001 (first entry)
XX	
DE	Nucleotide sequence of human gp39 protein, a CD40 ligand.
XX	
KW	gp39; CD40 ligand; osteoblast cell death; apoptosis; bone loss;
KW	osteoporosis; osteonecrosis; inflammatory arthritis; estrogen loss;
KW	ovariectomy; historectomy; lupus nephritis; Takayasu's arteritis;
KW	Wegener's granulomatosis; nephritis; myositis; scleroderma;
KW	thrombocytopenia; asthma; lung disease; cancer; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	22..807
FT	/tag= a
FT	/product= "gp39"
XX	
PN	WO200116180-A2.
XX	
PD	08-MAR-2001.
XX	
XX	
PF	24-AUG-2000; 2000MO-US23276.
XX	
PR	27-AUG-1999; 99US-0151250.
XX	
PA	(TEXA ) UNTV TEXAS SYSTEM.
XX	
PI	Ahuja SS, Bonewald LF;

XX WPI: 2001-169007/17.  
 DR P-PSDB: AAB67612.  
 XX  
 PT CD40 agonist containing composition, used to reduce bone cell death or  
 PT apoptosis associated with osteoporosis, osteonecrosis and inflammatory  
 PT arthritis -  
 XX  
 PS Disclosure: Page 113; 118pp; English.

CC The present sequence encodes a gp39 protein. It is a CD40 ligand.  
 CC CD40 ligands are used for reducing osteoblast cell death or apoptosis,  
 CC and for treating or preventing bone loss in animals, preferably humans,  
 CC at risk of, or undergoing, bone loss. The bone loss is associated with  
 CC osteoporosis, osteonecrosis, inflammatory arthritis, post-menopausal  
 CC oostrogen loss, estrogen loss due to ovariectomy, total hysterectomy,  
 CC lupus nephritis, Takayasu's arteritis, Wegener's granulomatosis,  
 CC anti-glomerular basement membrane nephritis, myositis, scleroderma,  
 CC idiopathic autoimmune thrombocytopenia, asthma, a chronic obstructive  
 CC lung disease, nephrotic/nephritic syndrome, or cancer. They may also be  
 CC used to treat or prevent bone loss in a subject undergoing, or scheduled  
 CC for, an organ or bone marrow transplant.

Sequence 879 BP; 274 A; 193 C; 190 G; 222 T; 0 other:

## Query Match

Best Local Similarity 46.4%; Score 720.2; DB 22; Length 879;  
 Matches 722: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 795 atggcaccatgaaggtgtgacacagatagaagaatgaaaggaatcttcacgaatttttat 854  
 DB 155 atcttcataagagtgtagcagacagatagaagaatgaaaggaatcttcacgaatttttat 854  
 QY 855 tcatgaaacagatagacagatgacacacagagaagaatccttactcctgaactgtg 914  
 DB 215 tcatgaaacagatagacagatgacacacagagaagaatccttactcctgaactgtg 914  
 QY 915 aggaattaaagcaggttgaaggttgaaggtatgaatgaatgaatgaatgaatgaatgaat 974  
 DB 275 aggaattaaagcaggttgaaggttgaaggtatgaatgaatgaatgaatgaatgaatgaat 974  
 QY 975 cgaagaagaagaacaggttgaatgacacacagatgacacacagatgacacacagatgacacac 1034  
 DB 335 cgaagaagaagaacaggttgaatgacacacagatgacacacagatgacacacagatgacacac 1034  
 QY 1035 atgtcataagtgagcagcagatgaacacacacatgtgtacagtggtggtggtggtggtggtggt 1094  
 DB 395 atgtcataagtgagcagcagatgaacacacacatgtgtacagtggtggtggtggtggtggtggt 1094  
 QY 1095 actacacacatgac 1154  
 DB 455 actacacacatgac 1154  
 QY 1155 gacacagactcttatatctatctatctatctatctatctatctatctatctatctatctatctat 1214  
 DB 515 gacacagactcttatatctatctatctatctatctatctatctatctatctatctatctatctat 1214  
 QY 1215 gtcaagctcattatagcagcagcctctcctcctcctcctcctcctcctcctcctcctcctcctc 1274  
 DB 575 gtcaagctcattatagcagcagcctctcctcctcctcctcctcctcctcctcctcctcctcctc 1274  
 QY 1275 tactcagacgtcacaataccac 1334  
 DB 635 tactcagacgtcacaataccac 1334  
 QY 1335 tgggagagatattatgacacacaggt 1394  
 DB 695 tgggagagatattatgacacacaggt 1394  
 QY 1395 gcccaag-gagcattgacacacaggt 1454  
 DB 755 gcccaagtgagcattgacacacaggt 1454

QY 1455 cactctgacgt 1514  
 DB 815 cactctgacgt 874  
 QY 1515 gccca 1519  
 DB 875 gccca 879

RESULT 2  
 AAA51745  
 ID AAA51745 standard: cDNA; 1816 BP.  
 XX  
 AC AAA51745;  
 XX  
 DT 31-OCT-2000 (first entry).  
 XX  
 DE Human CD40 ligand cDNA.  
 XX  
 KW CD40 ligand; CD40; T cell; T cell receptor; rearrangement; maturation;  
 KW cell death inhibition; stress-induced; immunosuppressive; anti-thyroid;  
 KW anti-inflammatory; anti-diabetic; anti-rheumatic; anti-anemic;  
 KW dermatological; cytoskeletal; nephrotrophic; hepatotropic; virucide;  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 40..825  
 FT FT /\*tag= a  
 FT FT /product= Human\_CD40\_ligand

MO200039283-A1:  
 PD 06-JUL-2000.  
 PD  
 PF 22-DEC-1999; 99MO-US30930.  
 PR 29-DEC-1998; 98US-0114106.  
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.  
 PI  
 PI PI  
 DR  
 DR WPI: 2000-452387/39.  
 DR P-PSDB; AAY96993.  
 PT Inducing T cell receptor gene rearrangement for treating autoimmune  
 PT diseases comprises contacting T cells with a CD40-binding agent  
 XX  
 PS Disclosure: Page 46; 50pp; English.

CD40 engagement on T cells can be used to induce T cell receptor  
 CC rearrangement and enhance T cell affinity for a particular antigen. CD40  
 CC engagement can be brought about by contacting CD40 with a CD40-binding  
 CC agent, e.g. human CD40 ligand. The CD40-binding agents can also be used  
 CC in methods for promoting T cell maturation, inhibiting T cell receptor  
 CC rearrangement, inhibiting environmental stress-induced cell death,  
 CC altering the specificity of a T cell towards an antigen, inducing T cell  
 CC reactivity towards an antigen or enhancing environmental stress-induced  
 CC cell death (all claimed). T cell affinity maturation towards a specific  
 CC antigen can be inhibited, especially for a self-antigen in an autoimmune  
 CC disease, which includes rheumatoid arthritis, rheumatic fever, insulin-dependent  
 CC diabetes mellitus, haemolytic anaemias, rheumatic fever, Crohn's disease,  
 CC Guillain-Barre syndrome, psoriasis, thyroiditis, Grave's disease,  
 CC myasthenia gravis, glomerulonephritis, autoimmune hepatitis or systemic  
 CC lupus erythematosus. Inducing environmental stress-induced T cell death  
 CC is carried out in a cancerous T cell or a self-reactive T cell where the  
 CC environmental stress is a chemotherapeutic agent (claimed).  
 XX  
 XX Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other:



XX  
SQ Sequence 840 BP; 263 A; 182 C; 181 G; 214 T; 0 other;

Query Match	43.9%	Score 681.2;	DB 19;	Length 840;
Best Local Similarity	99.6%	Pred. No. 8.2e-178;		
Matches 683; Conservative	0;	Mismatches 2		

QY	795	atgagcattgaaggtctgacaaagatagaagaatgaagaagatcttcaatgaagatttgat	85
Db	155	actcttcattgaaggtctggaacaaagatagaagaatgaagaagatcttcaatgaagatttgat	214
QY	855	tcatgaanaacgatacagaagatgacaaacagagaagaagatccctatccctactgaactgtg	914
Db	215	tcatgaanaacgatacagaagatgacaaacagagaagaagatccctatccctactgaactgtg	274
QY	915	aggagattaaagccgactttggaaggtctgtgaagatatatgtcttaacaaagaagaga	974
Db	275	aggagattaaagccgactttggaaggtctgtgaagatatatgtcttaacaaagaagaga	1034
QY	975	cgaagaaagaanaacagctttgtaaatgcanaaagrgatccagatccccaattgcygcac	1033
Db	335	cgaagaaagaanaacagctttgtaaatgcanaaagrgatccagatccccaattgcygcac	1093
QY	1035	atgtcatalaagtgaagccagacagataaacaacatctgtgtacagtgtggtctgaanaagat	1094
Db	395	atgtcatalaagtgaagccagacagataaacaacatctgtgtacagtgtggtctgaanaagat	1154
QY	1095	actacacccatgagacaaacaaacttgtaaccctgtgaanaatgggaacacgctgaacgttataa	1155
Db	455	actacacccatgagacaaacaaacttgtaaccctgtgaanaatgggaacacgctgaacgttataa	1215
QY	1155	gacaaagactctattatatactatgtgcccaagtcacactctgtcttccaatgggaagcttcga	1214
Db	515	gacaaagactctattatatactatgtgcccaagtcacactctgtcttccaatgggaagcttcga	1274
QY	1215	gtccaaactccattatagaacagctctctgcgttaagatcccccgttagatccgaagaaact	1274
Db	575	gtccaaactccattatagaacagctctctgcgttaagatcccccgttagatccgaagaaact	1334
QY	1275	tactcagagctgcgaaatccccacagttccgcgcaaacctgtcgggacaaatccattcaact	1334
Db	635	tactcagagctgcgaaatccccacagttccgcgcaaacctgtcgggacaaatccattcaact	1394
QY	1335	tggggaggtatttgaatttgcacaacaggtgtcttcggtgttttcaatgtgtgattccaa	1394
Db	695	tggggaggtatttgaatttgcacaacaggtgtcttcggtgttttcaatgtgtgattccaa	1454
QY	1395	gtccaaagtgaacgacgtgaactgttcaagttcctgttggttactcaaaactctgaacagtgt	1454
Db	755	gtccaaagtgaacgacgtgaactgttcaagttcctgttggttactcaaaactctgaacagtgt	1514
QY	1455	caacttgcagctgtgtgtgaactga	1480
Db	815	caacttgcagctgtgtgtgaactga	1540

RESULT	5
AA057984	
ID	AA057984 standard; DNA; 840 BP.
XX	
AC	AA057984;
XX	
DT	20-AUG-1994 (first entry)
XX	
DE	Genomic sequence of human gp39.
XX	
KW	gp39; T-cell antigen; CD40 ligand; B-cell proliferation.
KW	B-cell differentiation; ss.
XX	
OS	Homo sapiens.
XX	
PH	
Key	Location/Qualifiers



FT CDS 22..807  
 FT /tag= a  
 XX EP585943-A.  
 XX  
 PD 09-MAR-1994.  
 XX  
 PF 03-SEP-1993: 93EP-011A153.  
 XX  
 PR 04-SEP-1992: 92US-0940605.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 PI Aruffo AA, Hollenbaugh D, Ledbetter JA, Aruffo A;  
 XX WPI: 1994-076264/10.  
 DR P-PSDB; AAR59548.  
 PT New nucleic acid encoding human gp39 T cell antigen - which is a  
 PT ligand for the CD40 receptor, causing proliferation and  
 PT differentiation of B cells and some cancer cells  
 PS  
 PS Claim 1: Fig 1: 39pp; English.  
 CC The complete nucleic acid sequence of human gp39 (hgp39) protein  
 CC (corresp. to CDNA) and the complete AA sequence of hgp39 are  
 CC presented in AA057984 and AAR49548 respectively and contd. In plasmid  
 CC CD40-hgp39, deposited with the ATCC as E. coli, CD40 MC1061/P3-hgp39  
 CC and assigned accession No. 69050. The human T cell antigen gp39 is a  
 CC ligand for the CD40 receptor. Soluble gp39 may be produced using the  
 CC expression vector CD8-gp39.  
 CC  
 SQ Sequence 840 BP: 263 A; 180 C; 183 G; 214 T; 0 other;

Query Match 43.8%; Score 679.6; DB 15: Length 840;  
 Best Local Similarity 99.4%; Pred. No. 2,3e-177;  
 Matches 682; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 795 atggcattgaagagcttggaacagatgaagaatgaagaatcttcgaagattctgtat 854  
 DB 155 atctcattgaagagcttggaacagatgaagaatgaagaatcttcgaagattctgtat 214  
 QY 855 tcatgaaacagatgaagaatgaagaatgaagaatcttcgaagattctgtat 914  
 DB 215 tcatgaaacagatgaagaatgaagaatgaagaatcttcgaagattctgtat 274  
 QY 915 aggaagcttaaaagcagcttggaagcttggaagatataatcttaaaagagagaga 974  
 DB 275 aggaagcttaaaagcagcttggaagcttggaagatataatcttaaaagagagaga 334  
 QY 975 cgaagaagaagaacagcttggaatgcgaagaagtgatcagaatctcgaatcgagcac 1034  
 DB 335 cgaagaagaagaacagcttggaatgcgaagaagtgatcagaatctcgaatcgagcac 394  
 QY 1035 agtctaaagtgtgagcagcagtaaaacacatctgttaccagctgtgagcgaagaagat 1094  
 DB 395 agtctaaagtgtgagcagcagtaaaacacatctgttaccagctgtgagcgaagaagat 454  
 QY 1095 actacacacatgagcagaacattgttaacctgtggaatgaagaagcgtcagcgtcaaaa 1154  
 DB 455 actacacacatgagcagaacattgttaacctgtggaatgaagaagcgtcagcgtcaaaa 514  
 QY 1155 gacaaggaacttatatactatgcgaagtcgaactctgttcgaatcggaagcttgcga 1214  
 DB 515 gacaaggaacttatatactatgcgaagtcgaactctgttcgaatcggaagcttgcga 574  
 QY 1215 gtcagaagctcattatagcagcctgtcgaagtcgaagtcgaagtcgaagtcgaagtc 1274  
 DB 575 gtcagaagctcattatagcagcctgtcgaagtcgaagtcgaagtcgaagtcgaagtc 634  
 QY 1275 tactcagagctgcaaataccacagctcgcgaagcttgaggcgaacaatccattcact 1334

DB 635 tactcagagctgcaaataccacagctcgcgaagcttgaggcgaacaatccattcact 694  
 QY 1335 tggagagagatattgaatgcgaacacagctgctcggtgtgttcgaatgtgacgtaccaa 1394  
 DB 695 tggagagagatattgaatgcgaacacagctgctcggtgtgttcgaatgtgacgtaccaa 754  
 QY 1395 gccaagtgagcagctgagcagctgcttcgaactcttggaactacacaaacttggaagctg 1454  
 DB 755 gccaagtgagcagctgagcagctgcttcgaactcttggaactacacaaacttggaagctg 814  
 QY 1455 caccctgcagagctgtgtgagctga 1480  
 DB 815 caccctgcagagctgtgtgagctga 840

RESULT 6  
 ID AA041506  
 XX AA041506 standard; DNA; 840 BP.  
 AC AA041506;  
 DT 12-AUG-1993 (first entry)  
 XX  
 DE CD40-L DNA.  
 KW Human; CD40-L; CD40; type II; membrane; polypeptide; extracellular;  
 KW transmembrane; region; intracellular; soluble; activity; B cell;  
 KW proliferation; induction; antibody; secretion; IGE; agonist;  
 KW antagonist; binding assay; ss.  
 OS Homo sapiens.

EH key Location/Qualifiers  
 FT CDS 46..831  
 FT /tag= a  
 PN MO9308207-A.  
 XX  
 PD 29-APR-1993.  
 XX  
 PF 23-OCT-1992: 92MO-US08990.  
 XX  
 PR 25-OCT-1991: 91US-0783707.  
 PR 05-DEC-1991: 91US-0805723.  
 XX  
 PA (IMMUNEX ) IMMUNEX CORP.  
 XX  
 PI Amltalge RJ, Fanslow WC, Spriggs MK;  
 XX WPI: 1993-152417/18.  
 DR P-PSDB; AAR36701.  
 XX  
 PT New cytokine CD40-L as CD40 agonist and antagonist - is used for  
 PT treating allergies, lupus, rheumatoid arthritis,  
 PT graft-versus-host disease and insulin-dependent diabetes mellitus  
 PS  
 PS Claim 1: Fig 2: 80pp; English.

XX This sequence encodes a human CD40-L polypeptide which binds to CD40.  
 CC CD40-L is a type II membrane polypeptide which has an extracellular  
 CC region at its C-terminus, a transmembrane region and an  
 CC intracellular region at its N-terminus. A soluble form of CD40-L  
 CC lacks the transmembrane domain. CD40-L activity is mediated by  
 CC binding with CD40 an dinduces B cell proliferation and induction of  
 CC antibody secretion, including IGE. Membrane bound CD40-L acts as a  
 CC CD40 agonist and soluble CD40-L acts as a CD40 antagonist. CD40-L  
 CC can be used in a binding assay to detect cells expressing CD40.  
 XX  
 SQ Sequence 840 BP: 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match 42.3%; Score 657.2; DB 14: Length 840;  
 Best Local Similarity 99.5%; Pred. No. 3.4e-171;



Db 659 taccagagctgtcaaatatccacaagcttcgcacaaaccttgaggaggaataatccattcaact 718

Oy 1335 tggagagagatttgtaattgcacaaccaggtgctcggtgttgcacatgtagctgaccca 1394

Db 719 tggagagagatttgtaattgcacaaccaggtgctcggtgttgcacatgtagctgaccca 778

Oy 1395 gccaaagtgagccattgctcattgcttcaagtccttcttggtcttactcaaacctcgaaacagtg 1454

Db 779 gccaaagtgagccattgctcattgcttcaagtccttcttggtcttactcaaacctcgaaacagtg 838

Oy 1455 ca 1456

Db 839 ca 840

RESULT 8

AAT93782

AAT93782 standard; cDNA: 840 BP.

AAT93782:

16-FEB-1998 (first entry)

cDNA of CD40L, a novel cytokine ligand for CD40.

Cytokine: activated CD4+ T cell; CD40; CD40L; monoclonal antibody; neoplastic cell proliferation; B-cell lymphoma; immune deficiency; AIDS; melanoma; carcinoma; ss.

Homo sapiens.

Key Location/Qualifiers

CD5 46..831

FT CDS /tag= a

XX US5674492-A.

PD 07-OCT-1997.

XX 21-DEC-1994; 94US-0360923.

XX 23-DEC-1993; 93US-0172664.

PR 23-DEC-1993; 93US-0172664.

XX

PA (IMMUNEX CORP.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX

Amlicage RJ, Fanslow WC, Longo DL, Murphy WJ;

DR WPI; 1997-502273/46.

DR P-PSDB; AAMW34669.

XX

PT CD40-expressing cells - particularly B-cell lymphoma, by

PT administration of CD40-binding protein, preferably antibody or

PT soluble CD40-ligand

XX

Claim 3; Columns 19-22; 21pp; English.

XX

CC The present sequence represents the cDNA sequence of a novel cytokine

CC ligand for CD40 called CD40L. CD40L is a type II membrane polypeptide,

CC which is expressed by activated CD4+ T cells, and causes B cell

CC proliferation and induction of antibody secretion. The protein can be

CC used to produce monoclonal antibodies, which in turn bind to

CC CD40-expressing cells. This inhibits binding of soluble CD40 to its

CC ligand CD40L. The monoclonal antibody against CD40L is used to inhibit

CC proliferation of neoplastic cells, and is particularly useful in treating

CC B-cell lymphoma (e.g. where induced after transplants or in other cases

CC of immune deficiency such as AIDS), and also melanoma or carcinoma. Since

CC the monoclonal antibodies inhibit neoplastic cells directly, they may not

CC need to be coupled to a toxin or radioisotope, avoiding toxic effects on

CC normal B cells.

XX

Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match	Similarity	99.5%	Pred. No. 3.4e-171	Matches 659	Conservative	0	Mismatches	3	Indels	0	Gaps	0
QY	795	atgcacatcagaaaggtctggagacagaaatagaagaatgaaaggaaatctcatcagaaagattttgat	854									
Db	179	atcttcacatagaaggtctggagacagaaatagaagaatgaaaggaaatctcatcagaaagattttgat	238									
QY	855	tcatcagaaacagatlaacagagatgcaacacacagagagaaagatctctatccttaccgaaactgtg	914									
Db	239	tcatcagaaacagatlaacagagatgcaacacacagagagaaagatctctatccttaccgaaactgtg	298									
QY	915	aggagattcaaaagccaggtttgaaagccttctgtgaagagatataatgcttataacaaagagagga	974									
Db	299	aggagattcaaaagccaggtttgaaagccttctgtgaagagatataatgcttataacaaagagagga	358									
QY	975	cgaagaagaagaaacacagctcttgaaatgcaaaaagatgatacagaatccctcaaatctgcgcac	1034									
Db	359	cgaagaagaagaaacacagctcttgaaatgcaaaaagatgatacagaatccctcaaatctgcgcac	418									
QY	1035	atgctataaagtgaagccagacgaataaaacaacatctcgttgtataacagggcttgaaaaagagat	1094									
Db	419	atgctataaagtgaagccagacgaataaaacaacatctcgttgtataacagggcttgaaaaagagat	478									
QY	1095	actaacacacatgagcacaacaaactgtgtaaaccttgaaaccttggaaaaatgggaaaacagctgtcaaaa	1154									
Db	479	actaacacacatgagcacaacaaactgtgtaaaccttgaaaccttggaaaaatgggaaaacagctgtcaaaa	538									
QY	1155	gacaaagagatcattatatactatactatagcccaagatcaactctctgtctccaaatcgggaaagcttga	1214									
Db	539	gacaaagagatcattatatactatactatagcccaagatcaactctctgtctccaaatcgggaaagcttga	598									
QY	1215	gtcaagatcccatattataagcagaacctctgcgtctaagaatcccccggatagatctcgaagaatctc	1274									
Db	599	gtcaagatcccatattataagcagaacctctgcgtctaagaatcccccggatagatctcgaagaatctc	658									
QY	1275	tactcagaagctgcaaatatacccaacagatctccgccaacacctgtcgggcagaacaaatccatctact	1334									
Db	659	tactcagaagctgcaaatatacccaacagatctccgccaacacctgtcgggcagaacaaatccatctact	718									
QY	1335	tggggaggagattattgaattgcaacacagagtgctgggtgtgtttgtccaatgtagatgtccaa	1394									
Db	719	tggggaggagattattgaattgcaacacagagtgctgggtgtgtttgtccaatgtagatgtccaa	778									
QY	1395	gtcaagatgagccatgagcactgtgctcacaagctctctgtgcttaactcaaaactctgaacagtgct	1454									
Db	779	gtcaagatgagccatgagcactgtgctcacaagctctctgtgcttaactcaaaactctgaacagtgct	838									
QY	1455	ca 1456										
Db	839	ca 840										
Result 9												
AA227525												
ID AA27525 standard; cDNA; 840 BP.												
XX AA27525;												
XX 13-DEC-1999 (first entry)												



Sequence 840 BP: 266 A; 184 C; 174 G; 213 T; 3 other:

Query Match 42.28; Score 654.2; DB 18; Length 840;  
Best Local Similarity 99.1%; Pred. No. 2, 2e-170;  
Matches 656; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 795 atggcctatgaaggttgagcaagatagaagaatgaaagaaatcttcagaagatttctat 854  
DB 179 atctctatgaaggtctgagcaagatagaagaatgaaagaaatcttcagaagatttctat 238  
QY 855 tcatgaaagacatgacagatgacacacagagagaagaatcttcactgaactgctg 914  
DB 239 tcatgaaagacatgacagatgacacacagagagaagaatcttcactgaactgctg 298  
QY 915 aggaagattaaagcagcttggaagctcttggaagataatgataaacaagaagaga 974  
DB 299 aggaagattaaagcagcttggaagctcttggaagataatgataaacaagaagaga 358  
QY 975 cgaagaaagaaacagcttggaatgcaaaaaggctgataatccctcaattggcgac 1034  
DB 359 cgaagaaagaaacagcttggaatgcaaaaaggctgataatccctcaattggcgac 418  
QY 1035 atgtcataagtgagcgacagatgaacaacacatctgtctacagtgaggcgtaaaagat 1094  
DB 419 atgtcataagtgagcgacagatgaacaacacatctgtctacagtgaggcgtaaaagat 478  
QY 1095 actacacatgagcaacaacttgataacctggaanaatgggaacagctgacgttaaa 1154  
DB 479 actacacatgagcaacaacttgataacctggaanaatgggaacagctgacgttaaa 538  
QY 1155 gacaaagagctcttatatctatgacaaatgcacctctcttcacatcggaagcttga 1214  
DB 539 gacaaagagctcttatatctatgacaaatgcacctctcttcacatcggaagcttga 598  
QY 1215 gtcaagctcatctatataagcagctctgcctaaagctcccggtagatctgaaggaatc 1274  
DB 599 gtcaagctcatctatataagcagctctgcctaaagctcccggtagatctgaaggaatc 658  
QY 1275 tactcagagctgcacaataaccacagctccgcaaaactctgcgggcaacaatccatcact 1334  
DB 659 tactcagagctgcacaataaccacagctccgcaaaactctgcgggcaacaatccatcact 718  
QY 1335 tgggaagagatgtaattgcaaacagtgctcgcgtggttgcataatgtaactgatac 1394  
DB 719 tgggaagagatgtaattgcaaacagtgctcgcgtggttgcataatgtaactgatac 778  
QY 1395 gccaagtgagcagatgagcagctgcagctcctctgcttactcaaaacttgaaagatg 1454  
DB 779 gccaagtgagcagatgagcagctgcagctcctctgcttactcaaaacttgaaagatg 838  
QY 1455 ca 1456  
DB 839 ca 840

RESULT 11

AA094091  
ID AA094091 standard: cDNA; 840 BP.

XX  
AC AA094091;

XX  
DT 26-DEC-1995 (first entry)

XX  
DE Human CD40-L cDNA.

XX  
KM CD40 ligand; CD40-L; B-cell lymphoma; melanoma; carcinoma; ss.

XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers

FT CDS 46..831  
/\*tag- a

XX  
PN MO9517202-A1.

XX  
PD 29-JUN-1995.

XX  
PF 21-DEC-1994; 94MO-US14767.

XX  
PR 23-DEC-1993; 93US-0172664.

XX  
PA (IMM) IMMUNEX CORP.

XX  
PI Amlidge RJ, Fanslow WC, Longo DL, Murphy WJ;

XX  
DR WPI: 1995-240471/31.

XX  
DR P-PSDB: AAR76125.

XX  
PT Treating or preventing cancers where cells express CD40 - esp.

XX  
PS B-cell lymphoma, by treatment with a CD40 binding protein

XX  
PS Disclosure: Page 19-20; 34pp; English.

XX  
CC CD40-L is a type II membrane protein whose activity, mediated by

XX  
CC binding of its extracellular region to CD40, includes B-cell

XX  
CC proliferation and induction of antibody (including IgE) secretion.

XX  
CC CD40-L/FC2 fusion protein, trimeric CD40-L (33-amino acid zipper,

XX  
CC 8-amino acid hydrophilic sequence and the extracellular region of

XX  
CC CD40-L), and other forms of CD40-L can be produced by recombinant

XX  
CC methods. CD40-L cDNA has been cloned from peripheral blood

XX  
CC T-cells.

SO Sequence 840 BP: 266 A; 183 C; 176 G; 215 T; 0 other:

Query Match 42.08; Score 652.4; DB 16; Length 840;  
Best Local Similarity 99.1%; Pred. No. 7e-170;  
Matches 656; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 795 atggcctatgaaggttgagcaagatagaagaatgaaagaaatcttcagaagatttctat 854  
DB 179 atctctatgaaggtctgagcaagatagaagaatgaaagaaatcttcagaagatttctat 238  
QY 855 tcatgaaagacatgacagatgacacacagagagaagaatcttcactgaactgctg 914  
DB 239 tcatgaaagacatgacagatgacacacagagagaagaatcttcactgaactgctg 298  
QY 915 aggaagattaaagcagcttggaagctcttggaagataatgataaacaagaagaga 974  
DB 299 aggaagattaaagcagcttggaagctcttggaagataatgataaacaagaagaga 358  
QY 975 cgaagaaagaaacagcttggaatgcaaaaaggctgataatccctcaattggcgac 1034  
DB 359 cgaagaaagaaacagcttggaatgcaaaaaggctgataatccctcaattggcgac 418  
QY 1035 atgtcataagtgagcgacagatgaacaacacatctgtctacagtgaggcgtaaaagat 1094  
DB 419 atgtcataagtgagcgacagatgaacaacacatctgtctacagtgaggcgtaaaagat 478  
QY 1095 actacacatgagcaacaacttgataacctggaanaatgggaacagctgacgttaaa 1154  
DB 479 actacacatgagcaacaacttgataacctggaanaatgggaacagctgacgttaaa 538  
QY 1155 gacaaagagctcttatatctatgacaaatgcacctctcttcacatcggaagcttga 1214  
DB 539 gacaaagagctcttatatctatgacaaatgcacctctcttcacatcggaagcttga 598  
QY 1215 gtcaagctcatctatataagcagctctgcctaaagctcccggtagatctgaaggaatc 1274  
DB 599 gtcaagctcatctatataagcagctctgcctaaagctcccggtagatctgaaggaatc 658  
QY 1275 tactcagagctgcacaataaccacagctccgcaaaactctgcgggcaacaatccatcact 1334  
DB 659 tactcagagctgcacaataaccacagctccgcaaaactctgcgggcaacaatccatcact 718

Query Match	41.8%;	Score 648.2;	DB 15;	Length 786;
Best Local Similarity	99.5%;	Pred. No. 9.8e-169;		

01-DEC-1997;	97US-0982272.
09-DEC-1996;	96US-0032145.
08-DEC-1997;	97MO-US22740.

	RESULT	13
AAV38997	ID	AAV38997 standard; DNA; 786 BP.
XX		
AC	AAV38997;	
XX		
DT	23-SEP-1998	(first entry)
DE		
XX		
KW	CD40 ligand gene used in the course of the invention.	
KW	CD40 ligand; alteration; immunoreactivity; human cell;	
KW	accessory molecule ligand; AM; gene therapy; treatment;	
XX	autoimmune disorder; rheumatoid arthritis; vaccine; ss.	
OS	Mus sp.	
XX		
PN	MO9826061-A2.	
PN		
XX		
PD	18-JUN-1998.	
XX		
PF	08-DEC-1997;	97WO-US22740.
XX		
PR	01-DEC-1997;	97US-0982272.
PR	09-DEC-1996;	96US-0032145.
XX		
PA	(REGC ) UNIV CALIFORNIA.	



```

Db 314 cgaagaaagaaacacgcttgaataagcaaaaaggtgtaatcgaatccccaattgcgcac 373
OY 1035 atgcatagagagagcagcagtaaaacaacatcgtcttaccagtggcctgaaagat 1094
Db 374 atgcatagagagagcagcagtaaaacaacatcgtcttaccagtggcctgaaagat 433
OY 1095 actacacatagacacacacttgtaaccttgaaatgggaaacagctgaccgttaaa 1154
Db 434 actacacatagacacacacttgtaaccttgaaatgggaaacagctgaccgttaaa 493
OY 1155 gacagagacttatataatcattatgccaagtcacctctgttccaatcggaagcttga 1214
Db 494 gacagagacttatataatcattatgccaagtcacctctgttccaatcggaagcttga 553
OY 1215 gtcacagctcattatgacacagctctgcttaagtcacccggtgatcgagaatc 1274
Db 554 gtcacagctcattatgacacagctctgcttaagtcacccggtgatcgagaatc 613
OY 1275 tactcagagctgcaaatcaccacagcttcgcgaacaccttgcggaacaatccact 1334
Db 614 tactcagagctgcaaatcaccacagcttcgcgaacaccttgcggaacaatccact 673
OY 1335 tggagagagatattgtaattgcaaccagtgctcggtgttgcataatgtaactgaa 1394
Db 674 tggagagagatattgtaattgcaaccagtgctcggtgttgcataatgtaactgaa 733
OY 1395 gccagtgagcattgacatgcttgcacgtctcttgcgttaactaactctga 1447
Db 734 gccagtgagcattgacatgcttgcacgtctcttgcgttaactaactctga 786

RESULT 15
AAV39002
ID AAV39002 standard; DNA; 786 BP.
XX
AC AAV39002:
XX
XX 23-SEP-1998 (first entry)
XX
DE Exemplary CD40 ligand gene used in the course of the invention.
XX
KW CD40 ligand; alteration; immunoreactivity; human cell;
KW accessory molecule ligand; AMU; gene therapy; treatment; neoplasia;
KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
OS ChimERIC - Mus sp.
OS ChimERIC - Homo sapiens.
XX
XX W09826061-A2.
XX
XX 18-JUN-1998.
XX
XX 08-DEC-1997; 97WO-US22740.
XX
XX 01-DEC-1997; 97US-0982272.
XX
XX 09-DEC-1996; 9605-0032145.
XX
XX (REGC ) UNITV CALIFORNIA.
XX
XX Cantwell M, Kipps TJ, Sharma S;
XX
XX WPI: 1998-348521/30.
XX
XX Vectors containing accessory molecule ligand genes - used for
XX altering immunoreactivity of cells, particularly for treatment of
XX neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
XX
XX Disclosure: Page 106; 167pp; English.
XX
XX The present sequence represents an exemplary CD40 ligand gene,
XX comprising nucleotides encoding the extracellular domains (Domains III
XX and IV) and transmembrane domain (Domain II) of human CD40 ligand gene

```

```

CC (AAV38998) operatively linked to nucleotides encoding the cytoplasmic
CC domain (Domain I) of the murine CD40 ligand gene (AAV38997). The sequence
CC is used to exemplify the method of the invention. The specification
CC describes a method for altering the immunoreactivity of human cells which
CC comprises introducing a gene encoding an accessory molecule ligand (AMU)
CC into the cells so that the AMU is expressed on the surface of the cells.
CC Vectors containing the AMU genes can be used in gene therapy for
CC treating neoplasia or autoimmune disorders such as rheumatoid arthritis.
CC They can also be used for vaccination to produce immunity against a virus
CC cell, bacteria, protein, fungus or neoplasia.
XX
XX Sequence 786 BP: 250 A; 166 C; 171 G; 199 T; 0 other:

```

```

Query Match 41.8%; Score 648.2; DB 19; Length 786;
Best Local Similarity 99.5%; Pred. No. 9,8e-169;
Matches 650; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

OY 795 atgcatagagaggttgacagatagaagaatccttcaatgaaattgtat 854
Db 134 atcttcatagaaagcttgacagatagaagaatgaaagaaatccttcaatgaaattgtat 193
OY 855 tcatgaaacgatacagagatgcaacacagagaagaatccttcaatgaaattgtat 914
Db 194 tcatgaaacgatacagagatgcaacacagagaagaatccttcaatgaaattgtat 253
OY 915 agagattaaagcagattgaagcttctgtgaagataatgttaaaacaagagaga 974
Db 254 agagattaaagcagattgaagcttctgtgaagataatgttaaaacaagagaga 313
OY 975 cgaagaagaagaacagcttgtaaatgcaaaagtgatcagaatcccaatgagcgc 1034
Db 314 cgaagaagaagaacagcttgtaaatgcaaaagtgatcagaatcccaatgagcgc 373
OY 1035 atgcatagagagcagcagcagtaaaacaacatcgtgttacaagtggcctgaaagat 1094
Db 374 atgcatagagagcagcagcagtaaaacaacatcgtgttacaagtggcctgaaagat 433
OY 1095 actacacatagacacacacttgtaaccttgaaatgggaaacagctgaccgttaaa 1154
Db 434 actacacatagacacacacttgtaaccttgaaatgggaaacagctgaccgttaaa 493
OY 1155 gacagagacttatataatcattatgccaagtcacctctgttccaatcggaagcttga 1214
Db 494 gacagagacttatataatcattatgccaagtcacctctgttccaatcggaagcttga 553
OY 1215 gtcacagctcattatgacacagctctgcttaagtcacccggtgatcgagaatc 1274
Db 554 gtcacagctcattatgacacagctctgcttaagtcacccggtgatcgagaatc 613
OY 1275 tactcagagctgcaaatcaccacagcttcgcgaacaccttgcggaacaatccact 1334
Db 614 tactcagagctgcaaatcaccacagcttcgcgaacaccttgcggaacaatccact 673
OY 1335 tggagagagatattgtaattgcaaccagtgctcggtgttgcataatgtaactgaa 1394
Db 674 tggagagagatattgtaattgcaaccagtgctcggtgttgcataatgtaactgaa 733
OY 1395 gccagtgagcattgacatgcttgcacgtctcttgcgttaactaactctga 1447
Db 734 gccagtgagcattgacatgcttgcacgtctcttgcgttaactaactctga 786

```

Search completed: August 8, 2001, 05:59:53  
Job time: 4650 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleole - nucleole search, using sw model

Run on: August 8, 2001, 02:54:36 ; Search time 86.11 Seconds  
(without alignments)  
3412.041 Million cell updates/sec

Title: US-09-454-223-1

Perfect score: 1552  
Sequence: 1 gctagcggaattccaccacga.....aggcatgtagactcgtatcc 1552

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

ched: 324599 segs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgnl\_7/prodata/1/lna/5A\_COMB.seq:\*  
2: /cgnl\_7/prodata/1/lna/5B\_COMB.seq:\*  
3: /cgnl\_7/prodata/1/lna/5A\_COMB.seq:\*  
4: /cgnl\_7/prodata/1/lna/5B\_COMB.seq:\*  
5: /cgnl\_7/prodata/1/lna/5B\_COMB.seq:\*  
6: /cgnl\_7/prodata/1/lna/5B\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	681.2	43.9	840	1	US-07-940-605A-1
2	681.2	43.9	840	1	US-08-431-055-3
3	681.2	43.9	840	1	US-08-690-096-1
4	657.2	42.3	840	1	US-08-184-422-7
5	657.2	42.3	840	1	US-08-360-923A-1
6	657.2	42.3	840	2	US-08-249-189-11
7	657.2	42.3	840	2	US-08-484-624A-11
8	657.2	42.3	840	2	US-08-477-733B-11
9	657.2	42.3	840	3	US-08-763-995-1
10	657.2	42.3	840	3	US-09-088-913A-11
11	657.2	42.3	840	3	US-08-589-771B-7
12	648.2	41.8	786	5	US-08-446-922-3
13	648.2	41.8	786	5	PCT-US93-10034-3
14	638.6	41.1	1425	2	US-08-249-189-15
15	638.6	41.1	1425	2	US-08-484-624A-15
16	638.6	41.1	1425	2	US-08-477-733B-15
17	638.6	41.1	1425	2	US-09-088-913A-15
18	638.2	41.1	929	1	US-08-446-922-10
19	638.2	41.1	929	2	US-08-249-189-20
20	638.2	41.1	929	2	US-08-484-624A-20
21	638.2	41.1	929	3	US-08-477-733B-20
22	638.2	41.1	929	3	US-09-088-913A-20
23	462.8	29.8	818	1	US-08-431-055-1
24	456.2	29.4	783	1	US-08-446-922-5
25	456.2	29.4	783	2	US-08-249-189-1
26	456.2	29.4	783	2	US-08-484-624A-1
27	456.2	29.4	783	2	US-08-477-733B-1

28	456.2	29.4	783	3	US-09-088-913A-1	Sequence 1, Appl1
29	456.2	29.4	783	5	PCT-US93-10034-5	Sequence 5, Appl1
30	447.6	28.8	878	2	US-08-249-189-22	Sequence 22, Appl1
31	447.6	28.8	878	2	US-08-484-624A-22	Sequence 22, Appl1
32	447.6	28.8	878	2	US-08-477-733B-22	Sequence 22, Appl1
33	447.6	28.8	878	3	US-09-088-913A-22	Sequence 14, Appl1
34	186.6	12.0	342	5	PCT-US92-09955-14	Sequence 13, Appl1
35	168.6	10.9	325	5	PCT-US92-09955-13	Sequence 1, Appl1
36	129.2	8.3	1868	1	US-08-392-367B-1	Sequence 1, Appl1
37	129.2	8.3	1868	3	US-08-893-467A-1	Sequence 1, Appl1
38	124	8.0	3181	1	US-08-555-086-1	Sequence 20, Appl1
39	119.2	7.7	1881	4	US-09-029-348-20	Sequence 50, Appl1
40	117.2	7.6	756	1	US-08-642-255-50	Sequence 5, Appl1
41	116.6	7.5	1560	2	US-08-794-795-5	Sequence 5, Appl1
42	116.6	7.5	1560	4	US-09-249-200-5	Sequence 1, Appl1
43	116.6	7.5	1703	4	US-08-794-795-1	Sequence 1, Appl1
44	116.6	7.5	1703	4	US-09-249-200-1	Sequence 1, Appl1
45	105.6	6.8	810	1	US-08-642-255-60	Sequence 60, Appl1

## ALIGNMENTS

RESULT 1  
US-07-940-605A-1  
Sequence 1, Application US/07940605A  
Patent No. 5540926  
GENERAL INFORMATION:  
APPLICANT: ARUFPO, ALEJANDRO  
APPLICANT: HOLLEBAUGH, DINE  
APPLICANT: LEDBETTER, JEFFREY A.  
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/940,605A  
FILING DATE: 04-SEP-1992  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 5624-184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEO ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 22..807  
US-07-940-605A-1

Query Match 43.9%; Score 681.2; DB 1; Length 840;  
Best Local Similarity 99.6%; Pred. No. 8.5e-178;  
Matches 683; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 795 atggccatagaaggttgacacagatagaagaatgaagaatcttcacatgaatttgat 854
Db 155 ATCTTCATGAAAGGTTGGACCAAGATGAAAGATGAAAGAACTTCATGAAAGATTTGTAT 214
QY 855 tcatgaagaacgtatagaatgaacacacagagaagaatcttcacatgaatttgat 914
Db 215 TCATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATG 274
QY 915 aggaatgaagaacgtatgaagaatgaagaatgaagaatgaagaatgaagaatgaaga 974
Db 275 AGGAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATG 334
QY 975 gcaagaagaagaacagcttgaagaatgaagaatgaagaatgaagaatgaagaatgaaga 1034
Db 335 CGAAGAAAGAAAGACCTTGAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATG 394
QY 1035 atgtcataagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1094
Db 395 ATGTCATAGTGAAGGCGACAGTAAACATCTGTGTACAGTGGGCTGAAAAAGAT 454
QY 1095 actacacatgaagcaacacacttgtaacccctggaagaatgaagaacagctgaaga 1154
Db 455 ACTACACATGAGCAACCACTTGTGTACAGTGGGCTGAAAAAGATGAAAGATGAAAGATG 514
QY 1155 gacaagagctctatactatactatactatactatactatactatactatactatact 1214
Db 515 GACAAAGACTCTATATATCTATGCCCAAGTCACTTGTGTACAGTGGGCTGAAAAAGATG 574
QY 1215 gtaagctcattatagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1274
Db 575 GTCAAGCTCATTTATATGACCACTTGTGTACAGTGGGCTGAAAAAGATGAAAGATG 634
QY 1275 tactcagagctgaacacacacacacacacacacacacacacacacacacacacacac 1334
Db 635 TACTCAGAGCTGCAAAATGACCAAGTTCGCGCAACCTTGTGTACAGTGGGCTGAAAAAGAT 694
QY 1335 tgggagagagcttgaagaatgaagaatgaagaatgaagaatgaagaatgaagaatgaaga 1394
Db 695 TGGGAGAGATTTTGAATGCAACAGTGTGCTTGTGTACAGTGGGCTGAAAAAGATG 754
QY 1395 gcaagaatgaacatgaacatgaacatgaacatgaacatgaacatgaacatgaacatgaac 1454
Db 755 GCCAAATGAGCGCATGACAGTGTGCTTGTGTACAGTGGGCTGAAAAAGATG 814
QY 1455 caactcgaagcagctgctgagctga 1480
Db 815 CACCTGCGACGCTGTGTGAGCTGA 840

```

```

Sequence 3, Application US/08431055
Patent No. 5817516
GENERAL INFORMATION:
APPLICANT: KERRY, MERILYN R
APPLICANT: CASTLE, BRIAN E
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
NUMBER OF SEQUENCES: 4
DIFFERENTIATING B CELLS, AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,055

```

```

FLING DATE: 28-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,580
FLING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 22..807
US-08-431-055-3

```

```

Query Match 43.9% Score 681.2; DB 1; Length 840;
Best Local Similarity 99.6%; Pred. No. 8..5e-178;
Matches 683; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 795 atggccatagaaggttgacacagatagaagaatgaagaatcttcacatgaatttgat 854
Db 155 ATCTTCATGAAAGGTTGGACCAAGATGAAAGATGAAAGAACTTCATGAAAGATTTGTAT 214
QY 855 tcatgaagaacgtatagaatgaacacacagagaagaatcttcacatgaatttgat 914
Db 215 TCATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATG 274
QY 915 aggaatgaagaacgtatgaagaatgaagaatgaagaatgaagaatgaagaatgaaga 974
Db 275 AGGAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATG 334
QY 975 gcaagaagaagaacagcttgaagaatgaagaatgaagaatgaagaatgaagaatgaaga 1034
Db 335 CGAAGAAAGAAAGACCTTGAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATG 394
QY 1035 atgtcataagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1094
Db 395 ATGTCATAGTGAAGGCGACAGTAAACATCTGTGTACAGTGGGCTGAAAAAGAT 454
QY 1095 actacacatgaagcaacacacttgtaacccctggaagaatgaagaacagctgaaga 1154
Db 455 ACTACACATGAGCAACCACTTGTGTACAGTGGGCTGAAAAAGATGAAAGATGAAAGATG 514
QY 1155 gacaagagctctatactatactatactatactatactatactatactatactatact 1214
Db 515 GACAAAGACTCTATATATCTATGCCCAAGTCACTTGTGTACAGTGGGCTGAAAAAGATG 574
QY 1215 gtaagctcattatagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1274
Db 575 GTCAAGCTCATTTATATGACCACTTGTGTACAGTGGGCTGAAAAAGATGAAAGATG 634
QY 1275 tactcagagctgaacacacacacacacacacacacacacacacacacacacacacac 1334
Db 635 TACTCAGAGCTGCAAAATGACCAAGTTCGCGCAACCTTGTGTACAGTGGGCTGAAAAAGATG 694
QY 1335 tgggagagagcttgaagaatgaagaatgaagaatgaagaatgaagaatgaagaatgaaga 1394
Db 695 TGGGAGAGATTTTGAATGCAACAGTGTGCTTGTGTACAGTGGGCTGAAAAAGATG 754
QY 1395 gcaagaatgaacatgaacatgaacatgaacatgaacatgaacatgaacatgaacatgaac 1454
Db 755 GCCAAATGAGCGCATGACAGTGTGCTTGTGTACAGTGGGCTGAAAAAGATG 814

```

QY 1455 caccttcgaagctgtgtgagctga 1480  
|||||  
Db 815 CACCTTGACAGCTGTGTGTGAGCTGA 840

## RESULT 3

US-08-690-096-1  
; Sequence 1, Application US/08690096  
; Patent No. 5945513  
; GENERAL INFORMATION:  
; APPLICANT: ARUPFO, ALEJANDRO  
; APPLICANT: HOLLENBAUGH, DIANE  
; APPLICANT: LEDBETTER, JEFFREY A.  
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/690,096  
; FILING DATE: 31-JUL-1996  
; CLASSIFICATION: 536  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 07/940,605  
; FILING DATE: 04-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 5624-184  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 22..807  
; US-08-690-096-1

Query Match 43.9%; Score 681.2; DB 2; Length 840;  
Best Local Similarity 99.6%; Pred. No. 8.5e-178;  
Matches 683; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 795 atggccatgaaggttgagcaagatagaagatcgaagatcctcctgaagatttgat 854  
|||  
Db 155 ATCTTATAGAAAGCTTGACAAAGATAGAAAGATCAAGATCTTCTGAGATTGTTGTAT 214  
|||  
QY 855 tcatgaanagatagagagatgcaacacagagagaagatcctatcctactgaactgtg 914  
|||||  
Db 215 TCATGAAAGATGACATGACATGCAACACAGAGAAAGATCTTATCTTACTGAACTGTG 274  
|||||  
QY 915 agagagattaaagcaggttgagaggttgtagagagatataagttaaacaaagagaga 974  
|||||  
Db 275 AGAGAGTTAAAGCCAGTTTGAAGGCTTTGTGAGATATTAAGTTAAACAAAGAGAGACA 334  
|||||  
QY 975 cgagagaaagaaacagcttgaaatgcaaaagtgatcagaatcctcaaatgtcgagac 1034  
|||||

Db 335 CGAAGAAAGAAACACGCTTTGAATGCAAAAGGTGATCATGAATCTCAAAATTCGGCAGC 394  
QY 1035 agtcaataagtgagccagcagatgaataaacaacatctgtgttaagctgtgctgaaagagat 1094  
|||||  
Db 395 ATGTCAATAGTGAAGCCACAGAGTAAACAAATCTGTGTACAGTGGCTGAAAAGGAT 454  
QY 1095 actaacacatgaagcaacaaacttgtaaccttggaataatggaanagagcagaccgttaaaa 1154  
Db 455 ACTACACCATGACCAACAACTTGTTAACCTTGAAAATGGAAACAGCTGACCGTTAAAA 514  
QY 1155 gacaaagactctatatactatgcccagaagtcacctctgttccaaicgggaagcttga 1214  
|||||  
Db 515 GACAAAGACTATATATATCTATAGCCCAAGTGCATCTTGTTCCATTCGGGAAGCTTGA 574  
QY 1215 gtcaagctccattatagccagcctctgcttaagtcceccggtagatcagagaatct 1274  
|||||  
Db 575 GTCAAGCTCATTTATATAGCCAGCCTGCTTAAAGTCCCGTTAATTGCAAGAAATCT 634  
QY 1275 tactgaagctgcaaatataccaaagttccgccaaccttgcggggcaaaatccatccact 1334  
|||||  
Db 635 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAACCCTTGCGGCAACAAATCCATTCACT 694  
QY 1335 tggagagagatattgaaatgcaacacagtgctcgggtgttgcatactgactgacatccaa 1394  
Db 695 TGAGAGAGATATTGAAATGCAACAGAGTGCTTGGGTGTTGCATGTGACTGATCCAA 754  
QY 1395 gccaaagtgagcagtgagcagtgctcagtccttggtctactcaaacctcgaacagct 1454  
|||||  
Db 755 GCCAAAGTGAAGCCATGCGACGTGCTTCAGCTCTTGTGACTCAAACTGAAACAGTGT 814  
QY 1455 caccttcgaagctgtgtgagctga 1480  
|||||  
Db 815 CACCTTGACAGCTGTGTGTGAGCTGA 840

## RESULT 4

US-08-184-422-7  
; Sequence 7, Application US/08184422  
; Patent No. 5565321  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: DAVISON, BARRY  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: RENSNAW, BLAIR  
; APPLICANT: SPRIGGS, MELANIE  
; TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS  
; TITLE OF INVENTION: IN A CD40 LIGAND GENE  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: MS Word for Apple 5.1, Version a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/184,422  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/009,258  
; FILING DATE: 01/22/93  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PERKINS, PATRICIA ANNE  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2810-A  
; TELECOMMUNICATION INFORMATION:

RY	795	atracacattatcaaaccttttcccttc
RY Match	42.3%	Score 657.2; DB 1;
Local Similarity	99.5%	Pred. No. 3.3e-171;
Matches 659: Conservative	0; Mismatches	3; Indels 0; Gaps 0;

Db	179	ATCTTCATGAAAGGTTGGACAAGATGAAAGATGAAGAATCTTCATGAACATTTTGAT	238
Qy	855	tcattaaacagatcaagagatgcacaacagagagaagaatcccttacccttactgaactg	914
Db	239	TCATTAACAAACATACAGATGCAACACAGAGAAAGATCCTTATCTTACTGTAAACGTG	298
Qy	915	aggagatlaaaagccagatttgaaggtttgtgaagatataatgyltlaaacaaagaagaga	974
Db	299	AGGAGATTAAACGCAGTTTGAAGGCTTTGTGAAGATATATGTATTAACAAAGAGAGA	358
Qy	975	cgaagaaagaaacacagcttgaatgaatgcanaaagtgatcagatccctcaattgycgac	103
Db	359	CGAAGAAAGAAACACCTTTGAATGCAAAAAAGGTGATCAGATTCCTCAATTGCGCAC	418
Qy	1035	atgtcataagtgaagccagcagtaaacacacatctgtgttacgttggcttgaanaagat	1094
Db	419	ATGTCTAATGTTAGGCGCACACACTAAACAAATCTGTGTTCACGTGGCTGAAAAAGCAT	478
Qy	1095	actacaccatgtgcagaacacttgttaaccttgaaaatbvggaaacagctgcagcttaaa	1155
Db	479	ACTTACACATGAGCAACAACCTTGGTAACCTCGGAAAAATGGGAAACGTCGACCGTTAAA	538
Qy	1155	gacaaagactcattatatactatgcccgaagltcacctctgtcttccaatbvggaagcttga	1214
Db	539	GACAAAGACTCTATTATATATCTATCCCAAGTCAACCTTGTTCCAAATCGGAAAGTTTGA	598
Qy	1215	gtcaagctccattatagccagcctctgcgcttaagtcaccccgatgatctgagagaact	1274
Db	599	GTCAAGCTCCATTTATAGCCAGCCTCGCTTAAGTCCCCCGGTGATTCAGAGAAATCT	658
Qy	1275	tactcagagctgcnaatacccaacaafttcgcgaacacbtbvgcggcgaaacaatccact	1334
Db	659	TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAACAAATCCATTCCT	718
Qy	1335	tggaagagagatttgaatttgcacaacagtgcttgcgtgtgttgcacatbvgactatccaa	1394
Db	719	TGGGAGAGATTTTGAATTGCAACCAAGGTGCTTGGGTGTTCACATGTGACGTATCCAA	778
Qy	1395	gcacaagtgaagccatbvgcactgcttcaagctcttgggtttcttcaaacctbgaagtg	1454
Db	779	GCCAAAGTGAACCTGCGACATGGGTTCCAGTCTCTTTGGCTTACTCAAACTCTGAAACAGTGT	838
Qy	1455	ca 1456	
Db	839	ca 840	

APPLICANT: ARMITAGE, RICHARD  
APPLICANT: PANSLOW, WILLIAM  
APPLICANT: LONGO, DAN L.  
APPLICANT: MORPHY, WILLIAM  
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING  
TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS  
TITLE OF INVENTION: EXPRESSING CD40  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:

ADDRESS: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Apple Macintosh System 7.1  
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a  
CURRENT APPLICATION DATA:

FILING DATE: December 21, 1994  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 08/172,666  
 FILING DATE: December 23, 1993  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia A.  
 REGISTRATION NUMBER: 34,693  
 REFERENCE/DOCKET NUMBER: 2818-A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)233-0644  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:

```

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
-ORF-00-923A-1

```

Query Match	42.38;	Score 657.2;	DB 1;	Length 840;
Best Local Similarity	99.58;			
Matches 659; Conservative		Pred. NO. 3.3e-171;		

	CONSERVATIVE	Mismatches	Indels	Gaps
QY	795 atggccatagaaggttggacaagataagaatgtgaagaatctctatggaagttttgat	85	0	0
Db	179 ATCTTCATGAAAGGTTGGACAAAGATAGACAGTGAAGGAAATCTTCATGAAGATTTTGTAT	238		
QY	855 tcatgaacagataagatgacacacacagagaagaatctctatctactgaactgtg	914		
Db	239 TCATGAAAACGATTACAGAGATGCACACAGAGAAAGATCTTATCCTTACTGTAACAGTGTG	298		
QY	915 aggaagatlaaagccagtttgaagcctttggaagataaagttaacacaagaagagga	974		

```

|||||
Db 299 AGAGATTAAAGCCAGTTTGAAGCTTTGTGAGATATTAATGTTAAACAAAGAGAGACA 358
Qy 975 cgaagaagaagaacagcttgaatagaagaagaagtgatcaagaatcccaattcgagac 1034
Db 359 CGAAGAAACAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAAATGCGGCAC 418
Qy 1035 atgtcataagtagagccagcagtaaaacacactcgtgttacaagtaggctgaaaaagat 1094
Db 419 ATGTCTAATAGTAGCCACAGCTAAACAAACATCTGTGTACAGTGCGCTGAAAAGGAT 478
Qy 1095 actacacacatgaagcaaacacttgtaacctgtgaagaatggaagaacagctgacctaa 1154
Db 479 ACTACACCATGAGCAACAACCTTGTAACCTTGAAAATGGAACAGCTGACCGTTAAAA 538
Qy 1155 gacaaagactatataatcctatgcacaaagtcacacctctgtccaatcggaagcttga 1214
Db 539 GACAAAGCACTTATATATCTATGCCCAAGTCAACCTTGTTCAATCGGAAGCTTCGA 598
Qy 1215 gtcaagctcatcttataagcagccctctgtcctaaagtcaccccgtagatccagaagatc 1274
Db 599 GTCAAGCTCATTTATAGCACGCTCTGCTTAAAGTCCCGGTGATTCGAGAGATCT 658
Qy 1275 tactcagaagctgaacatacacaacagcttcgcaaaccttgcgagcaaatccatcact 1334
Db 659 TACTGAGACTGCAAAATACCAACAGTTCGGCAAACTTGCGGCAACAATCATTCAC 718
Qy 1335 tggagagagatattgaattgtaacagcagtgctcggtgtgttcaatgtacatgacaa 1394
Db 719 TGGAGAGATATTGTAATGCAACCAAGGTGCTGCGTGTGTGTAATGTGACATCCAA 778
Qy 1395 gccaaagtgacatgacatgacatgacatgacatgacatgacatgacatgacatgacat 1454
Db 779 GCCAAGTGAAGCATGACGACTGCTTACGCTTGGCTTACTCAAACTGTAACAGTGT 838
Qy 1455 ca 1456
Db 839 CA 840

```

```

RESULT 6
US-08-249-189-11
Sequence 11, Application US/08249189
Patent No. 5961974
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
TITLE OF INVENTION: NOVEL CYTOKINE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,189
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

```

```

APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
NAME/KEY: CDS
LOCATION: 46..831
US-08-249-189-11

```

```

Query Match 42.3%; Score 657.2; DB 2; Length 840;
Best Local Similarity 99.5%; Pred. No. 3,3e-171;
Matches 659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 795 atggccatagaaggttggaacagaatagaagaagaagaatccatcctgaaggtttgtat 854
Db 179 ATCTTCAATGAAAGTTTGCAAGATGAAAGATGAAAGCAATCTTCAATGAAATTTGTAT 238
Qy 855 tcatgaaacagatcacagagatgcaacacagaggaagaatccatccctacacagctgtg 914
Db 239 TCATGAAAACGATACAGAGATGCACACAGGAAAGATCTTATCTTACTGAACTG 298
Qy 915 aggaatataaaagcagcttggaagccttgtaagagataaaatgttaaaacaaagagaga 974
Db 299 AGGAGATTAAAGCCAGTTTGAAGGCTTGTGAGATATTAATGTTAAACAAAGAGAGACA 358
Qy 975 cgaagaagaagaacagcttgaatagaagaagaagtgatcagaatcccaatttggagac 1034
Db 359 CGAAGAAACAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAAATGCGGCAC 418
Qy 1035 atgtcataagtagagccagcagtaaaacacactcgtgttacaagtaggctgaaaaagat 1094
Db 419 ATGTCTAATAGTAGCCACAGCTAAACAAACATCTGTGTACAGTGCGCTGAAAAGGAT 478
Qy 1095 actacacacatgaagcaaacacttgtaaccttgtaagaatggaagaacagctgacctaa 1154
Db 479 ACTACACCATGAGCAACAACCTTGTAACCTTGAAAATGGAACAGCTGACCGTTAAAA 538
Qy 1155 gacaaagactatataatcctatgcacaaagtcacacctctgtccaatcggaagcttga 1214
Db 539 GACAAAGCACTTATATCTATGCCCAAGTCAACCTTGTTCAATCGGAAGCTTCGA 598
Qy 1215 gtcaagctcatcttataagcagccctctgtcctaaagtcaccccgtagatccagaagatc 1274
Db 599 GTCAAGCTCATTTATAGCACGCTCTGCTTAAAGTCCCGGTGATTCGAGAGATCT 658
Qy 1275 tactcagaagctgaacatacacaacagcttcgcaaaccttgcgagcaaatccatcact 1334
Db 659 TACTGAGACTGCAAAATACCAACAGTTCGGCAAACTTGCGGCAACAATCATTCAC 718

```

QY 1335 tggaggaatcttgatgcaacaggtgcttgcggtgttgcataatgctgacatccaa 1394  
 |||  
 Db 719 TGGAGGAGTATTGATTTGCAACAGGCTGCTGGTGTTCGAATGATGATGATGCA 778  
 |||  
 QY 1395 gccaaagtgaacatgagcactggtctgctcactgcttgcataaactgtgaacgtgt 1454  
 |||  
 Db 779 GCCAAGTAGCCATGGCAGCTGCTTCAAGTCTTGGCTTACTCAAACTGTGAACAGTGT 838  
 |||  
 QY 1455 ca 1456  
 ||  
 Db 839 CA 840

## RESULT 7

US-08-484-624A-11  
 : Sequence 11, Application US/08484624A  
 : Patent No. 5962406  
 : GENERAL INFORMATION:  
 : APPLICANT: ARMITAGE, RICHARD  
 : APPLICANT: FANSLAW, WILLIAM  
 : APPLICANT: SPRIGGS, MELANIE  
 : APPLICANT: SRINIVASAN, SUBHASHINI  
 : APPLICANT: GIBSON, MARYLOU  
 : APPLICANT: MORRIS, ARVIA E.  
 : APPLICANT: MCGREW, JEFFERY  
 : TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
 : NUMBER OF SEQUENCES: 26  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: IMMUNEX CORPORATION  
 : STREET: 51 UNIVERSITY STREET  
 : CITY: SEATTLE  
 : STATE: WASHINGTON  
 : COUNTRY: USA  
 : ZIP: 98101  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: Apple Macintosh  
 : OPERATING SYSTEM: Apple Operating System 7.5.5  
 : SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/484,624A  
 : FILING DATE:  
 : CLASSIFICATION:  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 08/477,733  
 : FILING DATE: June 07, 1995  
 : CLASSIFICATION:  
 : APPLICATION DATA:  
 : PRIOR APPLICATION NUMBER: 07/969,703  
 : FILING DATE: October 23, 1992  
 : CLASSIFICATION:  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 07/805,723  
 : FILING DATE: December 5, 1991  
 : CLASSIFICATION:  
 : APPLICATION DATA:  
 : APPLICATION NUMBER: 07/783,707  
 : FILING DATE: October 25, 1991  
 : CLASSIFICATION:  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Beckins, Patricia A.  
 : REGISTRATION NUMBER: 34,693  
 : REFERENCE/DOCKET NUMBER: 2802-D  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 2065870430  
 : TELEFAX: 2065870606  
 : INFORMATION FOR SEQ ID NO: 11:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 840 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: cDNA

HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 IMMEDIATE SOURCE:  
 CLONE: CD40-L  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 46..831  
 US-08-484-624A-11

Query Match  
 Best Local Similarity 42.3%; Score 657.2; DB 2; Length 840;  
 Matches 659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 795 atggccatagaaggttgagcaagatagaatgaagaatgaatcctcatgaagatttgat 854  
 |||  
 Db 179 ATCTCATGAAAGTTGGCAAGATGAAAGATGAAGAAATCTTCATGAAAGATTGTAT 238  
 |||  
 QY 855 tcatgaaacgatacagagatgcaacacaggaagaatccttacttacttactgtg 914  
 |||  
 Db 239 TATGAAACGATACAGAGATGCAACACAGSAGAAATCTTATCTTACTGAACTGTG 298  
 |||  
 QY 915 aggaattaaagccagcttgaaagcttggaaagtataatgttaaacaaagagaga 974  
 |||  
 Db 299 AGGAGATTAAAGCCAGTTTGAAAGCTTTGTGAAGTATTAATGTTAAACAAAGAGAGA 358  
 |||  
 QY 975 cgaagaaagaaagaaagcttggaaatgcaaaagtgatcagaatcctcattcgggac 1034  
 |||  
 Db 359 CGAAGAAAGAAACAGCTTTGAAATGCAAAAGTGATGATGATGATGATGATGATGAT 418  
 |||  
 QY 1035 atgtcataagtaggccaagcagtaaaacacatctgtgtacagtgggtgaaagagat 1094  
 |||  
 Db 419 ATGTCAATAGTAGAGCCAGCAGTAATAACATCTGTGTACAGTGGCTGAAAAAGAT 478  
 |||  
 QY 1095 actacacatgagcaacaactgtgtacccctggaatggaagcagtgacgttaaa 1154  
 |||  
 Db 479 ACTACACATGAGCAACACTGTGTACCCCTGAAAAATGGAAACAGTCAACCTTAAAA 538  
 |||  
 QY 1155 gacaagaactctatatactatgcccagtcacttctgttccaatggaagcctega 1214  
 |||  
 Db 539 GCAAGAGACTCTATATATCTATGCTATGCTCAAGTCACTTGTGTCCAAATGGGAACCTTGA 598  
 |||  
 QY 1215 gtaaacctcattatagccagcctctgcttaagctcccccgtagatctcagaagatc 1274  
 |||  
 Db 599 GTCAAGCTCATTATATGACCAACCTCTGCTTAAGTCCCGGTAGATTCGAGGAATCT 658  
 |||  
 QY 1275 tactcagagctgcaaatccacagtlccgccaaccttgcgggcaacaatccact 1334  
 |||  
 Db 659 TACTCAGAGCTGCAAAATACCAAGTTCCGCCAACCCTTGGGCCAACAATCCATTCACT 718  
 |||  
 QY 1335 tggaggaatcttgatgcaacaggtgcttgcggtgttgcataatgctgacatccaa 1394  
 |||  
 Db 719 TGGAGGAGTATTGATTTGCAACAGGCTGCTGGTGTTCGAATGATGATGATGCA 778  
 |||  
 QY 1395 gccaaagtgaacatgagcactggtctgctcactgcttgcataaactgtgaacgtgt 1454  
 |||  
 Db 779 GCCAAGTAGCCATGGCAGCTGCTTCAAGTCTTGGCTTACTCAAACTGTGAACAGTGT 838  
 |||  
 QY 1455 ca 1456  
 ||  
 Db 839 CA 840

## RESULT 8

US-08-477-733B-11  
 : Sequence 11, Application US/08477733B  
 : Patent No. 5981724  
 : GENERAL INFORMATION:  
 : APPLICANT: ARMITAGE, RICHARD  
 : APPLICANT: FANSLAW, WILLIAM  
 : APPLICANT: SPRIGGS, MELANIE

APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, ARVIA E.  
APPLICANT: MCGREM, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,733B  
FILING DATE: June 07, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/249,189  
FILING DATE: May 24, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-477-733B-11

Query Match 42.3%; Score 657.2; DB 2; Length 840;  
Best local similarity 99.5%; Pred. No. 3.3e-171;  
Matches 659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 795 atggcactagaaggttgagcaagaatagaagaatccttcataagattcgtat 854  
DB 179 ATCTTCATGAAGCTTGCACACATGAGATGAAAGCAATCTTCAAGATTGTAT 238  
QY 855 tcattgaacgatacagagatgcacacaggaagaatccttcataagattcgt 914

DB 239 TCATGAAAAGCATACAGATGCAACAGAGAAAGATCCTTACTACTACTG 298  
QY 915 aggaataaaagccagcttgaaagcttgtaagataaalytaaaacaaagagaga 974  
DB 299 AGGAGATTAAGCCAGTTTGAAGCTTTGTGAAGATATAATGTTAAACAAAGAGAGA 358  
QY 975 cgaagaagaagaacagcttgaaatgcaaaaaggtgatacgaatccttcataatggggc 1034  
DB 359 CGAAGAAAGAAAACAGCTTGAATGCAAAAGATATGAAATCTCAAAATGCCGAC 418  
QY 1035 atgcataagtgagccagcaagtaaaacaacatcgtgttacagtgaggctgaaagagat 1094  
DB 419 ATGTCAATTAAGTGAAGCCAGCAGCAAGTAAACAACTGTGTACAGTGGCTGAAAAAGCAT 478  
QY 1095 actacacactagcaacaacacttgtaacccttgaaaaatggaaacagctgaaacgttaaaa 1154  
DB 479 ACTACACCATGACCAACAACCTTGTAACTCGAAAATGGAAACAGCTGACCGTTAAAA 538  
QY 1155 gaaagagactctcttatctatagcccaagtcaccttcgttccaatcggaagcttga 1214  
DB 539 GACAAAGACTCTATTATATCTATGCCCCAAGTCACCTTGTTCAAATCGGAAGCTTCA 598  
QY 1215 gtcaagctccattatagcaagctctgctlaaagtcaccccgtagatcgaagaagatc 1274  
DB 599 GTCAAGCTCATTTATAGCAGCCTGTGCTTAAGTCCCGGTAACTTCGAGAGATGT 658  
QY 1275 tactcagaagctgcacaaatcccaagltccgcaaaccttgagggaacaacatccatcact 1334  
DB 659 TACTCAGACTGCCAATATACCACAGTTCGCGCAAACTTGGCGGCAACATCATTCACAT 718  
QY 1335 tggagagagattatgaattgcaaccaggtgctcggtgtttgcaatgagcagatccaa 1394  
DB 719 TGGAGAGAGATTGTAATGCACACAGGTGCTTGCTGTTGCAATGTGATGATCCAA 778  
QY 1395 gccaaatgagccatgagcactgctcagcttcacgttccttcactcaaacctgaaagatgt 1454  
DB 779 GCCAAATGAGCCATGGCAGCTGCTTACAGCTCTTTGGCTTACTCAAACTGTGAACGTGT 838  
QY 1455 ca 1456  
DB 839 CA 840  
RESULT 9  
US-08-763-995-1  
Sequence 1, Application US/08/63995  
Patent No. 6017527  
GENERAL INFORMATION:  
APPLICANT: MARASOVSKY, EUGENE  
TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Power Macintosh 7200/90  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/763,995  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/677,762  
FILING DATE: 10 JUL 1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2845-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
-763-995-1

Query Match 42.3% Score 657.2; DB 3; Length 840;  
Best Local Similarity 99.5% Pred. No. 3.3e-171;  
Matches 659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 795 atggccatgaaggttggcaagaatagaagatgaagatcttcagaaatttctat 854  
DB 179 ATCTTATAGAGGTTGGACAGATAGAAAGTAAAGAAAGATCTTCATGAAATTTGTAT 238  
QY 855 tcatgaaacgatatagagatgacacacagagagaagaatcccttaacctgaactgtg 914  
DB 239 TCATGAAACGATAGATGATGCAACACAGAGAAAGATCCTTATCCTTACTGACCTGT 298  
QY 915 aggaagattaaagccagtttgaaggttctgaaggtatataatgttaaaagaaggaga 974  
DB 299 AGGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGATATATGTTTAAACAAAGAGAGAG 358  
QY 975 cgaagaagaagaacagcttgaagatgcaaaaaggtgtcagaatccctcaaatctgcgac 1034  
DB 359 CGAAGAAAGAAACAGCTTCAAAATGCAAAAGGTGATGCAAAATCCTCAAAATGCGGAC 418  
QY 1035 atgtcataagtgagagcagcagatgaataaacacatctgtgtacagtgaggtgaaagat 1094  
DB 419 ATGTCATAGAGAGGCGCAGCACTAAACACATCTGTGTACAGTGGCTGAAAGAGAT 478  
QY 1095 actacacatgaggaacactgttaacctggaataatggaagaacagctgacgttaaaa 1154  
DB 479 ACTACACCATGAGCAACACTTGTAAACCTGGAATAATGGAAACAGCTGACCGTTAAA 538  
QY 1155 gacaagaccttatatctatctatgcccgaagtaaccttctgttcgaatcgggaagttcga 1214  
DB 539 GACAAGACACTCTATTATCTATGCCCCAAGTCACTTCTGTTCCAAATGGGAGAGCTTGA 598  
QY 1215 gtcaacctccattataagcagcctctgccttaaatctcccggtagatctgagaatct 1274  
DB 599 GTCAACCTCCATTATAGCCACCTCTGCTTAACCTCCCGGAGTAGATTCAGAGAAATCT 658  
QY 1275 tactcagagctgcaaataccacagttccgcgaacaccttgcgggaacaacatccattact 1334  
DB 659 TACTCAGACCTGCAAAATACCCACAGTTCGCGCAAACTGCGGCAACAAATCCATTACT 718  
QY 1335 tggagagagatttgaattgcaacaggtgtctcggtgttgcataatgtgactgataccaa 1394  
DB 719 TGGAGAGAGATTATTTGAATTCGAACAGGTGCTGCGGTGTGTCATATGTGACGATCAA 778  
QY 1395 gcccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1454  
DB 779 GCCAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 838

QY 1455 ca 1456  
DB 839 CA 840

RESULT 10  
US-09-088-913A-11  
Sequence 11, Application US/09088913A  
Patent No. 6087329  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSTON, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, ARVIA E.  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESS: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/088,913A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,624  
FILING DATE:  
APPLICATION NUMBER: 08/477,733  
FILING DATE: June 07, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-09-088-913A-11



Query Match 42.3%; Score 657.2; DB 3; Length 840;  
Best Local Similarity 99.5%; Pred. No. 3.3e-171;  
Matches 659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 795 atggccatagaagcttggagagatagaagaatccttcagaagatttgc 854  
Db 179 atcttcattagagcttgagacagatagaaagattcttcaagatttgc 238  
Qy 855 tcatgaagaaacagacagatgcacacagagagaatccctacctaactg 914  
Db 239 TCATGAAAGACATACAGATGCAACAGAGAAATCTTATCCTTACTGAC 298  
Qy 915 aggaattaaagcagcttgaagcttgcgaagataatgttaacaaagg 974  
Db 299 AGGAGATTAAAGCCAGCTTGAAGCGCTTGTGAAGCATATATGTTAA 358  
Qy 975 cgaagaaagaaacagcttggaaatgcaaaaagggtgcagaatcctca 1034  
Db 359 CGAAGAAAGAAACAGCTTGAATGCAAAAGGTGATCAGAAATCTCAAA 418  
Qy 1035 atgtcataagtgagccagcagtaaaacacatctgtctacagtgagc 1094  
Db 419 ATGTCATAAGTGAAGCCAGCAGTAAACATCTGTGTACAGTGGCGTGA 478  
Qy 1095 actacaccatgagcaaacacttggttaacccctggaaaacagctgac 1154  
Db 479 ACTACACCATGAGCAACACTTGTGTAACCTGGAATGGGAAACACTG 538  
Qy 1155 gaaagagactctatatctatctatgcagaaagtcagccctcttccaa 1214  
Db 539 GACAAAGACTCTATTATATATATGCCCCAAGTCACTTCTGTTCCAA 598  
Qy 1215 gtcaagctccatctatagcagcctctgcctaaagtcaccccgtaga 1274  
Db 599 GTCAAGCTCATATTATATGAGCCAGCTGTGCTTAAAGTCCCGGTA 658  
Qy 1275 tactcagagctgcgaataacacacagctgcgcaaaccttgcgggaa 1334  
Db 659 TACTCAGACCTGCAAAATACACAGTTCGCCCAAACTTGGGCAACAT 718  
Qy 1335 tggagagagcttctgaatctgaacccagtgctcgtgtgtgtcgaat 1394  
Db 719 TGGAGAGATTGATTTGATTCACACAGTGTGCTGCTTGTCAATGTCA 778  
Qy 1395 gccaagtgaagcctgagcctgctcagctccttgccttaactcaaac 1454  
Db 779 GCCAAGTGAACCATGGCAGTGGCTTCAAGTCTTGGCTTACTCAAA 838  
Qy 1455 ca 1456  
Db 839 CA 840

RESULT 11  
US-08-589-771B-7  
Sequence 7, Application US/08589771B  
Patent No. 6106832  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: DAVIDSON, BARRY  
APPLICANT: FANSHAW, WILLIAM  
APPLICANT: RENSHAW, BLAIR  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: WIDMER, MICHAEL  
TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING  
TITLE OF INVENTION: DEFECTIVE CD40L (as amended)  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE

STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS-DOS/Windows 95  
SOFTWARE: Word for Windows 95, 7.0a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/589, 771B  
FILING DATE: January 22, 1996  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/009, 258  
FILING DATE: 01/22/93  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HENRY, JAMES C.  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2810-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870606  
TELEFAX: 2065870430  
INFORMATION FOR SEQ. ID NO.: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-589-771B-7

Query Match 42.3%; Score 657.2; DB 3; Length 840;  
Best Local Similarity 99.5%; Pred. No. 3.3e-171;  
Matches 659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 795 atggccatagaagcttggagagatagaagaatccttcagaagatttgc 854  
Db 179 atcttcattagagcttgagacagatagaaagattcttcaagatttgc 238  
Qy 855 tcatgaagaaacagacagatgcacacagagagaatccctacctaactg 914  
Db 239 TCATGAAAGACATACAGATGCAACAGAGAAATCTTATCCTTACTGAC 298  
Qy 915 aggaattaaagcagcttgaagcttgcgaagataatgttaacaaagg 974  
Db 299 AGGAGATTAAAGCCAGCTTGAAGCGCTTGTGAAGCATATATGTTAA 358  
Qy 975 cgaagaaagaaacagcttggaaatgcaaaaagggtgcagaatcctca 1034  
Db 359 CGAAGAAAGAAACAGCTTGAATGCAAAAGGTGATCAGAAATCTCAAA 418  
Qy 1035 atgtcataagtgagccagcagtaaaacacatctgtctacagtgagc 1094  
Db 419 ATGTCATAAGTGAAGCCAGCAGTAAACATCTGTGTACAGTGGCGTGA 478  
Qy 1095 actacaccatgagcaaacacttggttaacccctggaaaacagctgac 1154  
Db 479 ACTACACCATGAGCAACACTTGTGTAACCTGGAATGGGAAACACTG 538  
Qy 1155 gaaagagactctatatctatctatgcagaaagtcagccctcttccaa 1214  
Db 539 GACAAAGACTCTATTATATATATGCCCCAAGTCACTTCTGTTCCAA 598

QY 1215 gtcagctccattatagccagcctctgctcctaagtcccccgtlagaattcgagaatct 1274  
DB 599 gtcagctccattatagccagcctctgctcctaagtcccccgtlagaattcgagaatct 1274  
QY 1275 tactcagagctgcgaataccacagcttcgcgaacacctgcgggcaacaatcattcaact 1334  
DB 659 tactcagagctgcgaataccacagcttcgcgaacacctgcgggcaacaatcattcaact 1334  
QY 1335 tggagagagatttgaattggaaccaggtgcttcggtgttctgaattgactgaccca 1394  
DB 719 tggagagagatttgaattggaaccaggtgcttcggtgttctgaattgactgaccca 1394  
QY 1395 gccagagagagctgcagctgcttcacgtccttgccttactcacaactgaacagtg 1454  
DB 779 gccagagagagctgcagctgcttcacgtccttgccttactcacaactgaacagtg 1454  
QY 1455 ca 1456  
DB 839 CA 840

US-08-446-922-3

Sequence 3, Application US/08446922  
Patent No. 5716805

GENERAL INFORMATION:

APPLICANT: Spriggs, Melanie

APPLICANT: Srinivasan, Subhashini

TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:

ADDRESS: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Apple Macintosh

SOFTWARE: Microsoft Word for Apple, Version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,922

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/107,353

FILING DATE: 08-13-93

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 1003-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 786 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Human

STRAIN: CD40-L

FEATURE:

NAME/KEY: CDS

LOCATION: 1..783  
US-08-446-922-3

Query Match 41.8%; Score 648.2; DB 1; Length 786;  
Best Local Similarity 99.5%; Pred. No. 9,5e-169;  
Matches 650; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 795 atgacatagaaagttgacacagatagaagaatgaagaatcattatgaagaattgac 854  
DB 134 ATCTCATAGAGAGTTGACACAGATAGAGATGAAGATCTTATGAAGATTGTAT 193  
QY 855 tcatgaaagaatgacagagatgacacagagagaaagatccttactcactgacgtg 914  
DB 194 TCAATGAAGATGACAGATGACACAGAGAAAGATCTTATCTTACTGAAGTGTG 253  
QY 915 aggaagattaaagccagtttgaaagcttgtaagatatatgttaacaagaagaga 974  
DB 254 AGGAGATTAAAGCCAGTTTGAAGCTTTGTAAGCATATATGTTAAACAAAGAGAGA 313  
QY 975 cgaagaagaagaacagcttgtaaatgcaaaaagtgatcagaatcctcaattgcgcac 1034  
DB 314 CGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGATGACAAATCTCAATTCCGCGAC 373  
QY 1035 atgtcataagtgagccagcaagtaaaacacatctgttgcagtggtgaaagaagat 1094  
DB 374 ATGCTAATAGTGAGCCAGCAGATGAACATCTGTGTACAGTGGCGTGAAGAAAGAT 433  
QY 1095 actacacatgagcaaacacttgtaacctggaanaatgggaacagctgaccgttaaa 1154  
DB 434 ACTACACATGAGCAACACTTGTGTACCTCGAANAATGGGAACAGCTGACCGTTAAA 493  
QY 1155 gacaagaactatatactatgccaagtcacacctgtgttccatcctggaaagcttga 1214  
DB 494 GACAAGACTCTATTATATATATATGATCCCAATCACTCTGTGTCAATCGGAAGCTTCA 553  
QY 1215 gtcagctccattatagccagcctctgctcctaagtcccccgtlagaattcgagaatct 1274  
DB 554 gtcagctccattatagccagcctctgctcctaagtcccccgtlagaattcgagaatct 1274  
QY 1275 tactcagagctgcgaataccacagcttcgcgaacacctgcgggcaacaatcattcaact 1334  
DB 614 TACTCAGAGCTGCGAATVACCACAGTTCGCGCAAACTTGGCGGCAACATCATCTACT 673  
QY 1335 tggagagagatttgaattggaaccagagtgcttggttgcataagtgactgaccca 1394  
DB 674 TGGAGAGAGATTGGAATTGCAACAGAGTGTGCTGTGTTGTCATGTGACTGACCA 733  
QY 1395 gccagtgagccatgagcactggtcctcactccttgccttactcacaactcga 1447  
DB 734 GCCAAGTGAGCCATGCGACTGCTTACAGTCTTGGCTTACTCAAACTCTGA 786

RESULT 13

PCT-US93-10034-3  
Sequence 3, Application PC/TUS9310034

GENERAL INFORMATION:

APPLICANT: Spriggs, Melanie

APPLICANT: Srinivasan, Subhashini

TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:

ADDRESS: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10034  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 1003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 786 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Human  
STRAIN: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..783  
PCT-US93-10034-3

Query Match 41.8% Score 648.2: DB 5: Length 786:  
Best Local Similarity 99.5% Pred.No.9.5e-169:  
Matches 650: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

Qy 795 atggccatagaaaggtgtgcaagaatgaaagaaatcttcagaaatttctglat 854  
Db 134 ATCTTCATAGAGTTGGACAGATGAAAGATGAAGATCTTCAATTTGTAT 193  
Qy 855 tcatgaaacgatacagaaatgcaacacaggaagaatccctacacgaattg 914  
Db 194 TCATGAAACGATACAGAGATGCAACAGAGAAAGATCTTATCTTACGAACTGTG 253  
Qy 915 aggaagatlaaaagccagcttgaaagcttctgaaagataatgttaaaacaaagagaga 974  
Db 254 AGCAGATTAAAGCCAGTTTGAAGCTTGTGAGAGATTAATGTTAAACAAAGAGAGA 313  
Qy 975 cgaagaagaagaacagcttgaatgcaaaaggtgatacagaatcccaaatctgcgac 1034  
Db 314 CGAAGAAAGAAAACAGCTTTGAATGCAAAAGGTGATCAGATCTCAATTGGCGCAC 373  
Qy 1035 atgtcataagtgagccagcagtaaaacacatctgtgttaacagtgagctgaaagaat 1094  
Db 374 ATGTCTAATAGTGGCCACAGTAAACAAACATCTGTGTACAGTGGCTGAAAAGGAT 433  
Qy 1095 actaacacacagcaacacacttgtaaccttgaaaaatgggaacacagctgaaccttaaaa 1154  
Db 434 ACTACACCATGACACAACTTGTGTAACCTTGAAAATGGAACAGCTGACCGTTAAAA 493  
Qy 1155 gacaaggactctatatactatgcaaaagtcacactctgttccaaatcggaagcttca 1214  
Db 494 GACAAGAGCTTATATATCTATGCCCCAAGTCACTTGTTCATTCGGGAAGCTTCA 553  
Qy 1215 gtcaagctcattatagcagcctctgtcctaaagtcaccccgtagatcagagaatct 1274  
Db 554 GTCAAGCTTCATTATAGCAGAGCTCTGCTAAAGTCCCGGTAACTTCGAGAGATCT 613  
Qy 1275 taactagagctgcaaaatcaccaagttccgcaaaccttgcgaggaacaaatccatcact 1334  
Db 614 TACTCAGAGCTGCAAAATACCAAGTTCGCGCAAACTTCGGGCAACATTCATTCACCT 673  
Qy 1335 tggagagaglatatgaattgcaaacagagtgctcggltgttctcaatgtcgaatccaa 1394  
Db 674 TGGAGAGATATTGAAATTGCAACAGAGTGTGGTGTTCATGTGACGATCCAA 733

Qy 1395 gccaaatgacatgacgactggttcacgtcttggcttactcaaaccttga 1447  
Db 734 GCCAAGTGAAGCATGGCAGCTGCTTACGCTTGGCTTACTCAAACTCTGA 786  
RESULT 14  
US-08-249-189-15  
Sequence 15, Application US/08249189  
Patent No. 5961974  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
TITLE OF INVENTION: NOVEL CYTOKINE  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/249,189  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1425 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: Human CD40-L/EC2 (soluble CD40-L)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 4..1422  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 79..1422  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 4..78



DB 885 GAACGTGTGACGAGATTAAAAAGCCAGTTTGAGGCTTTGTGAAGGATATATGTTAACAA 944  
QY 967 agagagagacgaagaagaagaacagcttgcgaatgcgaagaagtgatcagaatccccaat 1026  
DB 945 ACAGGAGAGCAAGAAAGAAACAGCTTTGMAATGCAAAAAGCTGATCAGAAATCTCAAAAT 1004  
QY 1027 tgcggcacaatgcataaagtgagagcagtgataaacaacactcgtgtacagtgagctga 1086  
DB 1005 TCGGGCACATGTGATTAAGTGAAGCCAGCAGTAAMACATCTGTGTACAGTGGCTGA 1064  
QY 1087 aaaaagatactacacacatgagcaacaacttggtaacctggaataatggaagaacagctgac 1146  
DB 1065 AAAGGATACCTACACCATGAGCAACAACCTTGGTAACCTGGAATAATGGGAACAGCTGAC 1124  
QY 1147 cgttaaaagaagaagactatatactatgcaccaagtcacctctcgttccaatcgga 1206  
DB 1125 CGTTAAACACAGGACTCTATTATATCTATGCCCCAAGTCACCTCTCTTCCAAATCGGGA 1184  
DB 1207 agcttcgagtcgaagctcaattatagccagctctgcctaaagtcccccgtagatlcga 1266  
DB 1185 ACCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCCCGGTAGATTGGA 1244  
QY 1267 ggaatcttaccagagctgcaaataccacaagtcgcgcaaaccttgcggcaacaatc 1326  
DB 1245 GAGAACTTACTCAGAGCTGCAAAATACCACAGTTCGCCAAACCTTGGGGCAACAATC 1304  
QY 1327 catcaacttggagaggatattgaaatgcacaacaggctgcgtggttltgtcaatgtgac 1386  
DB 1305 CATTCACCTGGAGAGGATTTGAATTGCAACAGGTGCTCGGTGTTGTCAATGTGAC 1364  
QY 1387 tgaatcaagccaaagtgaagcgaatgagcaatgcgttcacgttcacgttcacaaactcg 1446  
DB 1365 TGATCCAAAGCAAGTGAGCCATGSCATGGCTTCACGTCTTGCTTACTCAAACTCTG 1424  
QY 1447 a 1447  
DB 1425 A 1425

Search completed: August 8, 2001, 05:07:49  
Job time: 7993 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2001, 02:53:26 ; Search time 1594.91 Seconds  
(without alignments)  
9198.531 Million cell updates/sec

Title: US-09-454-223-1  
Perfect score: 1552  
Sequence: 1 gctgcgcgaattccaccacgga.....aggcatgtagaactgtaacc 1552

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

chod: 10228115 seqs, 4726426750 residues  
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
13: gb\_est13:\*  
14: gb\_est14:\*  
15: gb\_est15:\*  
16: gb\_est16:\*  
17: gb\_est17:\*  
18: gb\_est18:\*  
19: gb\_est19:\*  
20: gb\_est20:\*  
21: gb\_est21:\*  
22: gb\_est22:\*  
23: gb\_est23:\*  
24: gb\_est24:\*  
25: gb\_est25:\*  
26: gb\_est26:\*  
27: gb\_est27:\*  
28: gb\_est28:\*  
29: gb\_est29:\*  
30: gb\_est30:\*  
31: gb\_est31:\*  
32: gb\_est32:\*  
33: gb\_est33:\*  
34: gb\_est34:\*  
35: gb\_est35:\*  
36: gb\_est36:\*  
37: gb\_est37:\*  
38: gb\_est38:\*  
39: gb\_est39:\*  
40: gb\_est40:\*  
41: gb\_est41:\*  
42: gb\_est42:\*  
43: gb\_est43:\*

44: em\_esthum10:\*  
45: em\_esthum11:\*  
46: em\_esthum12:\*  
47: em\_esthum13:\*  
48: em\_esthum14:\*  
49: em\_esthum15:\*  
50: em\_esthum16:\*  
51: em\_esthum17:\*  
52: em\_esthum18:\*  
53: em\_esthum19:\*  
54: em\_esthum20:\*  
55: em\_esthum21:\*  
56: em\_esthum22:\*  
57: em\_esthum23:\*  
58: em\_esthum24:\*  
59: em\_esthum25:\*  
60: em\_esthum26:\*  
61: em\_esthum27:\*  
62: em\_esthum28:\*  
63: em\_esthum29:\*  
64: em\_esthum30:\*  
65: em\_esthum31:\*  
66: em\_esthum32:\*  
67: em\_esthum33:\*  
68: em\_esthum34:\*  
69: em\_esthum35:\*  
70: em\_esthum36:\*  
71: em\_esthum37:\*  
72: em\_esthum38:\*  
73: em\_esthum39:\*  
74: em\_esthum40:\*  
75: em\_esthum41:\*  
76: em\_esthum42:\*  
77: em\_esthum43:\*  
78: em\_esthum44:\*  
79: em\_esthum45:\*  
80: em\_esthum46:\*  
81: em\_esthum47:\*  
82: em\_esthum48:\*  
83: em\_esthum49:\*  
84: em\_esthum50:\*  
85: em\_esthum51:\*  
86: em\_esthum52:\*  
87: em\_esthum53:\*  
88: em\_esthum54:\*  
89: em\_esthum55:\*  
90: em\_esthum56:\*  
91: em\_esthum57:\*  
92: em\_esthum58:\*  
93: em\_esthum59:\*  
94: em\_esthum60:\*  
95: em\_esthum61:\*  
96: em\_esthum62:\*  
97: em\_esthum63:\*  
98: em\_esthum64:\*  
99: em\_esthum65:\*  
100: em\_esthum66:\*  
101: em\_esthum67:\*  
102: em\_esthum68:\*  
103: em\_esthum69:\*  
104: em\_esthum70:\*  
105: em\_esthum71:\*  
106: em\_esthum72:\*  
107: em\_esthum73:\*  
108: em\_esthum74:\*  
109: em\_esthum75:\*  
110: em\_esthum76:\*  
111: em\_esthum77:\*  
112: em\_esthum78:\*  
113: em\_esthum79:\*  
114: em\_esthum80:\*  
115: em\_esthum81:\*  
116: em\_esthum82:\*

117: gb\_est48:\*  
118: gb\_est49:\*  
119: gb\_est50:\*  
120: gb\_est51:\*  
121: gb\_est52:\*  
122: gb\_est53:\*  
123: gb\_est54:\*  
124: gb\_est55:\*  
125: gb\_est56:\*  
126: gb\_est57:\*  
127: gb\_est58:\*  
128: gb\_est59:\*  
129: gb\_est60:\*  
130: gb\_est61:\*  
131: gb\_est62:\*  
132: gb\_est63:\*  
133: gb\_est64:\*  
134: gb\_est65:\*  
135: gb\_est66:\*  
136: gb\_est67:\*  
137: gb\_est68:\*  
138: gb\_est69:\*  
139: gb\_est70:\*  
140: gb\_est71:\*  
141: gb\_est72:\*  
142: gb\_est73:\*  
143: gb\_est74:\*  
144: gb\_est75:\*  
145: gb\_est76:\*  
146: gb\_est77:\*  
147: gb\_est78:\*  
148: gb\_est79:\*  
149: gb\_est80:\*  
150: gb\_est81:\*  
151: gb\_est82:\*  
152: gb\_est83:\*  
153: gb\_est84:\*  
154: gb\_est85:\*  
155: gb\_est86:\*  
156: gb\_est87:\*  
157: gb\_est88:\*  
158: gb\_est89:\*  
159: gb\_est90:\*  
160: gb\_est91:\*  
161: gb\_est92:\*  
162: gb\_est93:\*  
163: gb\_est94:\*  
164: gb\_est95:\*  
165: gb\_est96:\*  
166: gb\_est97:\*  
167: gb\_est98:\*  
168: gb\_est99:\*  
169: gb\_est100:\*  
170: gb\_est101:\*  
171: gb\_est102:\*  
172: gb\_est103:\*  
173: gb\_est104:\*  
174: gb\_est105:\*  
175: gb\_est106:\*  
176: gb\_est107:\*  
177: gb\_est108:\*  
178: gb\_est109:\*

190: gb\_est110:\*  
191: gb\_est111:\*  
192: gb\_est112:\*  
193: gb\_est113:\*  
194: gb\_est114:\*  
195: gb\_est115:\*  
196: gb\_est116:\*  
197: gb\_est117:\*  
198: gb\_est118:\*  
199: gb\_est119:\*  
200: gb\_est120:\*  
201: gb\_est121:\*  
202: gb\_est122:\*  
203: gb\_est123:\*  
204: gb\_est124:\*  
205: gb\_est125:\*  
206: gb\_est126:\*  
207: gb\_est127:\*  
208: gb\_est128:\*  
209: gb\_est129:\*  
210: gb\_est130:\*  
211: gb\_est131:\*  
212: gb\_est132:\*  
213: gb\_est133:\*  
214: gb\_est134:\*  
215: gb\_est135:\*  
216: gb\_est136:\*  
217: gb\_est137:\*  
218: gb\_est138:\*  
219: gb\_est139:\*  
220: gb\_est140:\*  
221: gb\_est141:\*  
222: gb\_est142:\*  
223: gb\_est143:\*  
224: gb\_est144:\*  
225: gb\_est145:\*  
226: gb\_est146:\*  
227: gb\_est147:\*  
228: gb\_est148:\*  
229: gb\_est149:\*  
230: gb\_est150:\*  
231: gb\_est151:\*  
232: gb\_est152:\*  
233: gb\_est153:\*  
234: gb\_est154:\*  
235: gb\_est155:\*  
236: gb\_est156:\*  
237: gb\_est157:\*  
238: gb\_est158:\*  
239: gb\_est159:\*  
240: gb\_est160:\*  
241: gb\_est161:\*  
242: gb\_est162:\*  
243: gb\_est163:\*  
244: gb\_est164:\*  
245: gb\_est165:\*  
246: gb\_est166:\*  
247: gb\_est167:\*  
248: gb\_est168:\*  
249: gb\_est169:\*  
250: gb\_est170:\*  
251: gb\_est171:\*  
252: gb\_est172:\*  
253: gb\_est173:\*  
254: gb\_est174:\*  
255: gb\_est175:\*  
256: gb\_est176:\*  
257: gb\_est177:\*  
258: gb\_est178:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.





QY 614 ggtccaggaggt-cccccaagactcaaggaggagaggtgtctctggaagacagagaat 672  
 Db 601 ggtccaggagggccccccagagactcaaggaggagacagaggtgtctctggaagacagagaat 660  
 QY 673 caaaggtgaagaggggtctccagacagagtgctgtcagagagagatggaagcctaa 732  
 Db 661 caaaggtgaagaggggtctccagacagagtgctgtcagagagagatggaagcctaa 720  
 QY 733 aggaactacagaggtctcagaggtgtcctctccactacag-aaagctgactgtctc 791  
 Db 721 AGGAAACTACAGCCTCAGAGGTCCTCTCCACTATCAGAAAGCTGCATGTTCCTCC 780  
 QY 792 ctgtgtgacataagaaggttgacagaat 819  
 Db 781 CTGATGCCCGAAGTGTGAGACAGAT 808

RESULT 2  
 BFL40515 766 bp mRNA EST 24-OCT-2000  
 LOCUS 601787532P1 NCI\_CGAP\_Lu30 Mus musculus cDNA clone IMAGE:4015350 5',  
 DEFINITION mRNA sequence.  
 VERSION BFL40515.1 GI:10979542  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC http://mgi.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LHAM9260 row: p column: 07  
 High quality sequence stop: 745.  
 Location/Qualifiers  
 1..766  
 /organism="Mus musculus"  
 /strain="CZECH II"  
 /db\_xref="taxon:10090"  
 /clone\_image="IMAGE:4015350"  
 /clone\_lib="NCI\_CGAP\_Lu30"  
 /tissue\_type="tumor, metastatic to mammary"  
 /lab\_host="DH10B"  
 /note="Organ: Lung; Vector: pCMV-SPORT6; Site:1: NotI;  
 Site:2: SalI; transgenic model WNT-1, expression driven by  
 MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo  
 47. Library constructed by Life Technologies.  
 Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 190 a 186 c 254 g 136 t

Query Match 40.7%; Score 632; DB 145; Length 766;  
 Best Local Similarity 97.0%; Pred. No. 3.4e-166;  
 Matches 708; Conservative 0; Mismatches 15; Indels 7; Gaps 6;

QY 17 aggaagaaatcgaagatcgcctctctcactgtctgtctgtctgtacagccctg 76  
 Db 2 AGGAAGAAATCTGCCATGCTCCCTTCTCCATGCTGTGCTGTACAGCCCTG 61  
 QY 77 ggaagaaatcggagagaaatgaagagctctgcaagagatcagtaaccaactgac 136  
 Db 62 GGAAGATCTGGAGCAGAAATGAAGAGCTCTCCAGAGATCACTACCAACCTGCAC 121

QY 137 ctatcatgtttagcccaacagaagaatggtcctgtgtctgtatgtgaagagatgagga 196  
 Db 122 CTAGTCATGTGTAGCCCGACAGAGAAATGGCTGCTGTGTATGAGGAGATGGGAA 181  
 QY 197 gaaggtcaaggggtgaagaggtgatccaggtgttcagagacctatggtgtcagag 256  
 Db 182 GAAGGTCCACCGGGGTGAAGAGGTGATCCAGGTTTCCAGAGACTTATGSGGCTCTCAGG 241  
 QY 257 ttgcaagggccctacaggttcaatgtgaaccacaagagaagaatgtctgtgtgcaacct 316  
 Db 242 TTGCAAGGCCCTACAGTCCAGTTGACCCCAAGAGAGAAATGGCTGTCTGTGGCAACT 301  
 QY 317 ggaacaaaggaagagctgtgactaagtgaacctccagacctcagagratctctgtcca 376  
 Db 302 GGACCAAGGAGAGAGCTGACTAAGTGAAGTCCAGGACTTCCAGATATCTGTGTCCA 361  
 QY 377 gctggagaaaggtctccctctggaagagagagacat-aggacctcaagcaacagag 435  
 Db 362 GCTGGGAAGAGAGCTCTCTGGAAGCAGGGGAAACATTAAGACTCTCAAGCAACAGG 421  
 QY 436 tcttaagagagaggtgtggcccaagagaagatgtctctgtcatgtgaagatctac 495  
 Db 422 TCTTAAGAGAGAGCTGTGG-CCAAAGAGAGTACTGTCTCTGCAATGCAAGATCTAC 480  
 QY 496 agggcaaaaggtctccacagagggcccaagagaagagatgtccctgtgtgtcaagagc 555  
 Db 481 AGGGCAAAAGGCTCTCACAGGCCCCCAAGGAGACAGAGTCTCTGCTGTGCAAGAGC 540  
 QY 556 ccccaaggaaatgtctgaagacagagacctcgcagacctgcagagcaagagagctcagag 615  
 Db 541 CCCAGGAAATGCTGGGGAG-AGCACTGTGACCTGTGCTGTCCACAGAGGACTCCAGG 599  
 QY 616 ttccagagggcccccaagactcaaggaggagagaggtgtctcctgtgagacagagaaatcaa 675  
 Db 600 TTCCAGAGGGCCCCCAGAGACTC-AGGGGAGACAGAGTCTCTGTGAGACAGAGAAATCAA 658  
 QY 676 aggtgaagaggggtctccagacagtgctgtctgtgagcagacagatgagagcttaagag 735  
 Db 659 AGGTGACAGCGGCTCCACAGAGTG-TGCTGTGAGGACAGACAGTG-GGCCTTAAAGG 715  
 QY 736 aaactacag 745  
 Db 716 AAAACTACAG 725

RESULT 3  
 BFL181880 752 bp mRNA EST 31-OCT-2000  
 LOCUS 601805307P1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:4036393 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BFL181880  
 VERSION BFL181880.1 GI:11060022  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC http://mgi.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: Lohar Hemmighausen Ph.D., Robin Humphreys  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LHAM9311 row: m column: 02  
 High quality sequence stop: 673.

**FEATURES**  
**SOURCE**

Location/Qualifiers  
1. .752

```

/organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone_image="4036393"
/clone_lib="NCI CGAP_Mem5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: Saliv; Site_2: Nci1; Cloned unidirectionally. Primer: Oligo dT Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Nobin Humphreys, IHH"

```

BASE COUNT	200 a	180 c	252 g	120 t
ORIGIN				

**ORIGIN**

Query Match	40.18;	Score 622.2;	DB 145;	Length 752;
-------------	--------	--------------	---------	-------------

BEGL Local Similarity 94.38; Pred. NO. 1.9e-163/  
Matches 201; Conservative 0; Mismatches 23

Matches 701; Conservative 0; Mismatches 33; Indels 9; Gaps 5;

OY	12	ccacaggaagacaaactcgcacatgcctccctccacacagctctcctcctgacagc	71
Db	18	CAACAAGGAAGCAATCTGACATGCTGCCCTTCTCTCATGCTTGTCTTCTGTACAGC	77
OY	72	ccctcggaaactctggagacgaatctgaagacctctcgcagagatcagtaaccaacact	131
Db	78	CCCTGGGAAATCTGGAGACGAATGAAAGACCTCTGCGAGATCGTACCCMACCT	137
OY	132	gcacccctcagctatctgtatgagcccaacaaagaaatgagccctgctcgtcgtatgagacggatg	191
Db	138	GCACCCCTAGTATGTGTGAGCCCAACAAGAAATGGCCCTGCTGGTGTGATGAGACGGGATG	197
OY	192	ggagagaaagctccacagggctgtagaaggctgatccagctctgcagagacctaagggctc	251
Db	198	GGAGAGAAGGTCACAGGGGGTGAAGGGCTGATCCAGTTTGCCAGACACATGGGCGCTCT	257
OY	252	caaggtctgcagggccctacaggtcagctcgaacccaaagagaaatgctctgcgcg	311
Db	258	CAGGGTTGCAAGGGCCCTTACAGAGCTCCATTTGGACCCAAAGAGAAATGGCTCTGCTGGCG	317
OY	312	aacctggaccaaagggagaaacgtgactaagtgtgacctccagaaactccaggtatctcgt	371
Db	318	AACCTGGACCAAAAGGGAACGTGTGATTAAGTGAACCTCCAGACCTTCCAGGTATTTCTG	377
OY	372	gtccagactgggaagaaaggtccctcctctggaagcagggagaaataagacctccaaagcaac	431
Db	378	GTCACAGTGGGAAGGAAGGTCCCTCTGTGGAAAGCAAGGGCAACATAGACCTCAAGGCCAAC	437
OY	432	caaggtccaaagagaagagctcgggcccacaaagagaagtaagttgctctcctcgtcagaaat	491
Db	438	CAGTCTCTTAAAGGAGAGCTGTGGCCCAAAAGACAACTAGTGTGCTCCGTGCATGAAGAT	497
OY	492	ctacagagggcacaagagcttccacagggcccacaagagaagaaaggttgcctccgggtgtgaag	551
Db	498	CTACAGGGGCAAAAGG--TCCACAGAGCCCCCAAGGAGCAAAAGGTGCCCTCTGTGTGCAG	556
OY	552	gaagcccaaggaatgctcgaagcagcaaggaacctgcggagacctgcgcgttccacaggaagctc	611
Db	557	GAGCCCCAGGAATGCTGTGAGACACAGAC--TGCGAATCTGGGGTCCACAGGAAGCTC	613
OY	612	caaggtccaaaggggccccccaggaactaaaggggacagaagttgttccctcggagaacagga	671
Db	614	CAGGTTCCAGGGG--CCCCAGAGACTCAAGGGGGCAACAAGTGTTCCTGTGGACACAGAGAA	671
OY	672	tcaaaagtgaaagc-cgggtctccacagacgtctcctcctgcgaagcagcagataggaagcctaa	731
Db	672	TCACAGGTGA--GCGGGCTTCAAGACAGTGTCTCTCGGAAGCAG--ACAAGAGGGCTTAA	728
OY	732	aaggaataactacagcgtcctgagc 754	

Db 729 AGGAACTAAAGGGCTAAAAAG 751

[illegible]

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (pages 1 to 822)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished. (1999)  
Contact: Robert Strausberg, Ph.D.

## FEATURES

### Source

/organism="Mus musculus

/SLFALH=FVB/N

```
/usr/local/cuda0.1103  
/clone="IMAGE:4488260
```

```
/clone lib="NCI CGAP Mamm1"
```

```

/tissue_type="tumor, bloop

```

```
/dev_stage="3 months, virgin"
```

```
/lab_host="DH10B"
```

/note="Organ: m

site\_2: NCBI; cloned unidirectionally. Primer: origo database constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH

BASE COUNT	212 a	202 c	266 g	142 t
ORIGIN				

**ORIGIN**

Query Match	Score	DB	Length
39.88	618	175	822

Best Local Similarity 98.4%; Pred. No. 3e-16z;

Matches 677; Conservative 0; Mismatches 5; Indels 6; Gaps 5;

Qy	12	ccaccagaagaacatctacactgcctccctctctccacgcttgcttgcttgtaaacg	71
Db	13	CAACAAGAGAACAACTACATGCGCCCTTCTCTCATGCTTGTCTTGCTTGACAC	72
Qy	72	cccttggaaatcttggagcagaataatgaagagcctctctgcagagatcaagtaccacaacct	13
Db	73	CCCTGGAAATCTGGAGACAGAAATGAAGAGACCTCTCCAGAGATCAATACCAACACT	13
Qy	132	gcaccctatgtatgtgtgtcccaacaaagaatctgctccctgtgtgtatgtgaagggatg	19
Db	133	GCACCTGATGTCATGTGTATGTCGCCAAGAGAAATGGCTCTCCGTGTGATGACGGGATG	19
Qy	192	ggagagaagatccacaggggtgtagaagggctgataccaggtcttgccaggaactatagggctct	25
Db	193	GGAGAGAAGCTCCACGGGGGTGAGAAAGGGTGTATCCAGGTTCCACAGGACCTATGGGGCTCT	25
Qy	252	caaggtcttcagaaggccctcacaagtcacaagcttgaaaccacaagaaggagaaatgagctctctggcg	31
Db	253	CAGGGTTCCAGGGCCCTTACAGACTCCAGTTTGAAACCCMAAGAGAGAAATGGCTCTGCTGGCG	31
Qy	312	aacctgtgacccaagaaggagaaagcttgagactaaatggaacctccagaactccaggtatccctg	37

RESULT	5				
LOCUS	Bf101636				
DEFINITION	Bf:01636	739 bp	mRNA	EST	
ACCESSION	601753557F1	NCI-GAP_Maml	Mus musculus	cdna	clone IMAGE:3980846 5'
VERSION	Bf101636				
KEYWORDS	Bf101636.1	GI:10884162			
	EST.				

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Mus musculus					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; 1 (bases 1 to 739)					
NIH-MGC			<a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a>		
National Institutes of Health; Mammalian Gene Collection (MGC)					
Unpublished (1999)					
Contact: Robert Strausberg, Ph.D					

```

FEATURES      . . . . . sequence stop: 683.
source        1. .739      Location/Qualifiers

```

BASE COUNT	190 a	174 c	254 g	121 t
ORIGIN	Providing samples: Gilbert Smith, NIH			

Db	14	TGTACGCCCCCTGGGAATATCTGGGACACGAAGTAAGAACCCCTCTGCGAGATCATGATACC	73
QY	124	caaacacctgcacacctagatcaatgtatgtaaccacaagaaatgacctgacctgtgtgtgtg	183
Db	74	CACACCTCGCACCTTACTATCTATGTGTGTGCCCAACACAGAAATGGCTGCTGTCTGTATGG	133
QY	184	acggatgtggagagaagatgccacgggggttgagaaggtgtatccaaagtttgcacgaacctat	243
Db	134	ACGGGATGGGAGAGAAAGTTCACAGGGGGTGTAGAAAGGGTATACAGATGTTGCCACGACCTAT	193
QY	244	ggggctctcaagtttgtcagggccctacagtgctcagtttgacaccaagaagaaatgcttc	303
Db	194	GGGGCTCTCAGGGTTCACAGGGCCCTTACAGATGCTCAGATTGGACCCMAAGAGAAATGGCTC	253
QY	304	tgctggcgaacctcggacccaagggagaaactgtgactaagtgtgacctccagacttccag	363
Db	254	TGCTGGCGCAACCTGGACCCMAAGGAGAAAGTGTGACTAATGTGACCTCCAGGACTTCAGAG	313
QY	364	tattccttgctcaagcttgggaagaaggttcctctcgggaagcaagggagaaatagagacctca	423
Db	314	TATTCTGTGTTCCAGTGTGGAAAGAGGTCCTCTGGGAAGCAGGGAAATATAGGACTCA	373
QY	424	agggcaaaccaaggttccaaagagaaggtctggggcccaagaagagaagatagttgtctctgcat	483
Db	374	AGGCAAAACAGAGTCTCTTAAGGAGAGAGCTGGGGCCCAAAAGAGAAATGTGTCTCGGCAT	433
QY	484	ggcaagatctcaacagggcacaaggtctccacaggtccccaagggagagaagaaggtgtccctgg	543
Db	434	GCAAGGATCTACAGGGCCCAAAAGGCTTCCACAGGCCCCCAAGGAGAAATAGTGTCCCTCGG	493
QY	544	tgtgcaaggaagccccaaggaatgtcttgaaacagcaggaactgtccgaacctgtcgggttcaca	603
Db	494	TGTGCAAGGAGACCCCA-GGAATGCTGTGACACAGAGAGACTCG-CGGACTGTGGCGTCCACA	551
QY	604	gggaagctccaaagtttccaaaggggggcccacaggaact-aaagggagacaaggtgttctctggag	662
Db	552	GGGAGCTCCAGGTTCCAGGGGGCCCCCACAAGACTCAAAAGGGGACAGAGGTTCCTGTGAG	611
QY	663	acagaagaatcacaaggtgaagaacgggtctccagaagaagtgctcctctgaagccagacagtg	722
Db	612	ACAAGAGAACTCAAGGTGGAAGAGCGGGGTTCACAGAC-GCTGCTGTGAGGCAG-AGATGG	669
QY	723	agagcttaaaagaa	737
Db	670	GGGCTTTAAAGGAA	684

RESULT	6
BE382093	
LOCUS	
DEFINITION	BE382093 639 bp mRNA
ACCESSION	60127225F1 NCL_CGAP_Mam1 Mus
VERSION	BE382093 mRNA sequence.
KEYWORDS	BE382093
SOURCE	BE382093.1 GI:9327458
ORGANISM	EST.
	house mouse.
	Mus musculus
	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 639)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLM8787 row: 1 column: 13  
High quality sequence stop: 589.

## FEATURES

Location/Qualifiers  
1. 639

Source  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3601620"  
/clone\_lib="NCI\_CGAP\_Mam1"  
/tissue\_type="tumor, biopsy sample"  
/dev\_stage="3 months, virgin"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1; SalI;  
Site:2; NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigators  
providing samples: Gilbert Smith, NIH"  
BASE COUNT 157 a 160 c 214 g 108 t  
ORIGIN

Query Match 37.8%; Score 586.2; DB 166; Length 639;  
Best Local Similarity 99.2%; Pred. No. 2.2e-153;  
Matches 600; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

## FEATURES

Source  
1. 571  
/organism="Mus musculus"  
/strain="C57/B6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3481958"  
/clone\_lib="NCI\_CGAP\_Mam5"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1; SalI;  
Site:2; NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigators  
providing samples: Lothar Hennighausen/Robin Humphreys,  
NIH"  
BASE COUNT 144 a 143 c 189 g 95 t  
ORIGIN

Query Match 35.6%; Score 553.2; DB 166; Length 571;  
Best Local Similarity 99.1%; Pred. No. 3.9e-144;  
Matches 567; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

264 gccctacaggtcagcttgagcccaaaagagaaatgagctctgctgagaccttgagca 323  
241 gccctacaggtcagcttgagcccaaaagagaaatgagctctgctgagaccttgagca 300  
324 agggagaaagctgagctgagctgagctgagctgagctgagctgagctgagctgag 383  
301 accgagaaagctgagctgagctgagctgagctgagctgagctgagctgagctgag 360  
384 agggagaaagctgagctgagctgagctgagctgagctgagctgagctgagctgag 443  
361 agggagaaagctgagctgagctgagctgagctgagctgagctgagctgagctgag 420  
444 agggagaaagctgagctgagctgagctgagctgagctgagctgagctgagctgag 503  
421 gagagagctgagctgagctgagctgagctgagctgagctgagctgagctgagctgag 480  
504 agggagaaagctgagctgagctgagctgagctgagctgagctgagctgagctgag 563  
481 agggagaaagctgagctgagctgagctgagctgagctgagctgagctgagctgag 540  
564 agggagaaagctgagctgagctgagctgagctgagctgagctgagctgagctgag 623  
541 agggagaaagctgagctgagctgagctgagctgagctgagctgagctgagctgag 598  
624 agggagaaagctgagctgagctgagctgagctgagctgagctgagctgagctgag  
599 gggccc 603

RESULT 7  
BE336562 571 bp mRNA EST 14-JUL-2000  
LOCUS 601086764F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:3481958 5',  
DEFINITION mRNA sequence.  
ACCESSION BE336562  
VERSION BE336562.1 GI:9188953  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 571)  
NIH-MGC <http://mgc.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strusberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLM8510 row: 0 column: 15  
High quality sequence stop: 569.  
Location/Qualifiers  
1. 571  
/organism="Mus musculus"  
/strain="C57/B6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3481958"  
/clone\_lib="NCI\_CGAP\_Mam5"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1; SalI;  
Site:2; NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigators  
providing samples: Lothar Hennighausen/Robin Humphreys,  
NIH"  
BASE COUNT 144 a 143 c 189 g 95 t  
ORIGIN

34 gctgcctctctcctcagctgctgctgctgctgctgctgctgctgctgctgctgctg 93  
1 gctgcctctctcctcagctgctgctgctgctgctgctgctgctgctgctgctgctg 60  
94 aatgaagagctctcagcagagatcagctacccaaacacccctgacccctgacccctgac 153  
61 aatgaagagctctcagcagagatcagctacccaaacacccctgacccctgacccctgac 120  
154 aacagagaaatgagctgagctgagctgagctgagctgagctgagctgagctgagctgag 213  
121 aacagagaaatgagctgagctgagctgagctgagctgagctgagctgagctgagctgag 180  
214 gaaggagaaatgagctgagctgagctgagctgagctgagctgagctgagctgagctgag 273  
181 gaaggagaaatgagctgagctgagctgagctgagctgagctgagctgagctgagctgag 240  
274 tccagctgagaaag 333  
241 tccagctgagaaag 300  
334 tggactaaagtgaagctcagagctcagagctcagagctcagagctcagagctcagagctc 393

Db	301	TGSACTAGTGGACTCCAGACTTCCAGGTATTCCTGTGTCAGCTGGGAAAGAGTCC	360	
OY	394	ctctcgggaagcagggsaaca	tagaactccaagcaaaccaaggtcctcaagagagctcgg	453
Db	361	CTCTGGGAAAGCAGGGGAACATAGGACTCAAGCAAAACAGTCTCTAAAGGAGAGCTGG	420	
OY	454	gcccaaaaggaagaatgaatgctctctcgtgcattgcaagaa	cttacaagggcacaagaagctcac	513
Db	421	GCCCAAGGAGCAAGTACGTCCTCTCTGGACATGCACAAAGATCTACAGGGGCAAAAGGCTCCAC	480	
OY	514	agggcccaagsgaagaaaggtgccccctggtgtgcaagagagcccaaggaatgtctcgagc	573	
Db	481	AGGCCCCAAGGGAAGAAAGGTGCCCTCGTGTGCAAGAGAGCCCCAGGAAATGCTGGAGC	540	
OY	574	agcagagacctgcgcgacctgcgcggtccacaag	605	
Db	541	AGCAAGCACTGC--GGACTGCCGCTCCACAGG	570	

RESULT	B
BE370239	
DESCRIPTION	BE370239 537 bp mRNA EST 21-JUL-2000 601210777P1 NCI-CGAP_Lu29 Mus musculus cDNA clone IMAGE:359106 5'
ACCESSION	BE370239
VERSION	EST.
KEYWORDS	house mouse. Mus musculus
SOURCE	Mus musculus
ORGANISM	

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
1 (bases 1 to 537)  
NIH-MGC <http://mgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strushenski, Ph.D.

Email: cgaaps-remail.nl.nov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: <http://image.llnl.gov>  
plate: LMA8757 row: 1 column: 19  
High quality sequence stop: 537.

## FEATURES

BASE COUNT	137 a	130 c	182 g	88 t
ORIGIN	Providing samples: Gilbert			

Query Match	34.38;	Score 532.2;	DB 166;	Length 537;
Best Local Similarity	99.48;	Pred. No. 3e-138;		
Matches 534;	Conservative	0;	Mismatches	3.

Oy 48 ccatgctctgtcttgcctgtgtacagccctctggaaatcttgagcsgaaatgaagacctc 107  
 |||||  
 Db 1 CCATGCTTGTCTTGTGTACAGCCCTGGGAATCTGGAGCAGAATATAAGACCTC 111  
 |||||  
 Oy 108 cgcagatcactagttaccaacaccttgacccctagtcactgtgtagcccaacaggaatggcc 167  
 |||||

Db 61 CGCAGATCAGTACCCMACCTGCACCCCTGATATGTAGCCCGCAGAGTAAGGCC 120

Qy 168 tgcctgctcgtgatgagcaggatgaggagaaagtcacacgggctgagaaagtgatccag 227

Db 121 TGCTGTCTGTATGACGAGGATGGAGAGAAAGTCCACGGGGTGaAAGGTATCCAG 180

Qy 228 gtttcgcaggacctatgagggctcctaaggtttgcaggggccctacagtcacagtcgagcca 287

Db 181 GTTTGCCAAGACCTAAGGGGCTCTAGGGTTGACAGGCCCTACAGTCCAGTTGACCCA 240

Qy 288 aagagagaaatgctcctgctgtgcgaaccttgaaacaaagaggaagcgttgactaaagtgcac 347

Db 241 AAGACAGAAATGGCTCTGCTGCGCAACCTGGACCCAAAGGAGAAACGTGGACTAAGTGAC 300

Qy 348 ctccaggactccaggaattccttgctgcagcttggaagaagctccctcttggaagcag 407

Db 301 CTCACGAGATTCACAGTATTCCTGGTCCAGCTGGGAAGAAAGTCCCTCTGGGAAACAG 360

Qy 408 ggaacatggaacctcaagagcaaacaggctccctaagagagagcttgagcccaagagaag 467

Db 361 GGAATATAGGACCTCAAGGCAAAACAGAGTCTTAAAGAGAGCGCTGGGCCCAAGGAAAG 420

Qy 468 taagtgctccctcggcatgcaagagatctcaccagggcacaagagctccacagccccaaaggag 527

Db 421 TAGTGCTCTCGGATCCAAAGATCTTACAGGGGCAAAAGCTCCACAGCCCCCAAGGGAG 480

Qy 528 aaagagtgccccctggtgtgcgaagagccccaaagagatctgagccagcagagctgtg 584

Db 481 AAAAGAGGTGTCCTCGGTGTGTCAAGAGAGCCCAAGGAATCTGGGACACAGAGACTCG 537

RESULT	9
BG243812	
LOCUS	BG243812 530 bp mRNA
DEFINITION	6023537834F1 NC_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4486233 5'
ACCESSION	BG243812
VERSION	BG243812.1 GI:12753627
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 530).			
	NIH-MGC <a href="http://mgc.nhl.nih.gov/">http://mgc.nhl.nih.gov/</a> .			
	National Institutes of Health, Mammalian Gene Collection (MGC)			
	unpublished (1999)			
	Contact: Robert Strassburg, Ph.D.			

```

FEATURES
source      Location/Qualifiers
1. 530

```

Procurement: Gilbert Smith, Ph.D.  
Library Preparation: Life Technologies, Inc.  
Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
Sequencing by: Inqte Genomics, Inc.  
Distribution: MCC clone distribution information can be  
through the I.M.A.G.E. Consortium/LNL at:  
image.lnl.gov  
LNL0329 row: d column: 10  
Library sequence stop: 530.  
Location/Qualifiers  
1. 530  
/organism="Mus musculus"  
/strain="PVR/A"  
/db\_xref="taxon:10090"  
/clone\_image:448623"  
/clone\_id="NCI\_CGAP\_Mam1"  
/tissue\_type="tumor, biopsy sample"  
/dev\_stage="3 months, virgin"  
/lab\_host="DH10B"  
/note="Organ: mammary. Vector: PCMV-SPORT6. Site:1: Saliv  
Site-2: Nct1. Cloned unidirectionally. Primer: Oligo dr  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"



```

      trace: LLMM10256 row: n column: 22
      High quality sequence stop: 630.
      Location/Qualifiers
          1..980

```

```

/organism="Mus musculus"
/strain="PvB/N"
/db_xref="taxon:10090"
/clone_image="IMAGE:4458453"
/clone_1b="NCI CGAP Mam1"
/lssue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: PCMV-SPOB6; Site1: SalI; Site2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

```

	Query Match	30.9%	Score 479.8	DB 174	Length 980
	Best Local Similarity	88.6%	Pred. No. 2e-123		
	Matches 667	Conservative 0	Mismatches 72	Indels 14	Gaps 13
QY	12	ccaccaggaagcaatcgtacatgctgccctttccatcgtctgtctgttaacagc	71		
DB	10	CAACCAAGGAGCAATGTGACATGCTGCCCTTCTCTCCATGCTAGCTTGTTGACAC	69		
	72	cccttggaatctcggagacgaagaatgaabaagcctctcgagagatagtaacaaacct	131		
DB	70	CCCTGGGAAMTCTGGAGCAAGAAATGAAGGCTCTCCGAGAGATCAGTACCCAACACCT	131		
QY	132	gacccctatgcatgtgttagcccaacagagaatcggcctctggtcgtatgtagcggatg	191		
DB	130	GACCCCTTAATCTGTGTATGCTACCCCAACAGAAATGGCTGCTGCTGTGTAATGACGGATG	189		
QY	192	ggagagaagtcacacggggttagaagggtgtgataccaggtttgcaggacctatggggcct	251		
DB	190	GGAGAGAAGGTCACAGGGGTGAGAAAGGCTGATCCAGG-TTCCACAGGACCTTATGGGGCTCT	248		
QY	252	cagggtttgcaggggccctacaggttcaggttcaggttcaggttcaggttcaggttcaggttc	310		
DB	249	CAGGG-TGCAGGGCCCTTCAGGTCCAG-TGGACCCMAAGGACAAATGGCTCTCTGCGCA	306		
QY	311	gaaccttgaccaaaggaggaacgttgagactaagtggaccttcaggacttcaggatctc	370		
DB	307	GAACCTTGACCAAGGAGAACGTGGACTAATGTGACCTCCAGGACTTCAGGATATACCT	366		
QY	371	ggtcagcttgaggaaagaagtcctctctgggaagcaggaggagacatagagactcaagga	430		
DB	367	GGTCAACTGGGAAGAAGGCTCCTCTGGGAAGCAGGGAACATATAGCA-CTCAAGGCAAA	425		

[illegible]

## BE284648

LOCUS	BE2846648	553 bp	mRNA	EST	26-OCT-2000
DEFINITION	601087626F1 NCT_CGAF_Man5		musculus cDNA	clone IMAGE:3482431	5'
ACCESSION	BE2846648		mRNA sequence.		
VERSION	BE2846648				
KEYWORDS	BE2846648.1	GI:9161730			
SOURCE	EST.				
ORGANISM	house mouse.				
	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 653)				
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999)				
	Contact: Robert Struhsberg ph n				

**FEATURES**

**SOURCE**

```

/organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone_image="3482431"
/clone_id="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

```

Query Match

30.88; Score 478.2; DB 165; Length 653;



Best Local Similarity 97.1%; Pred. No. 4,7e-123;  
Matches 541; Conservative 0; Mismatches 8; Indels 8; Gaps 5;

```
QY 19 gaagcaatctgaatctgccccttcctccatgctgtcttgctgtaagccctcgg 78
    |||
Db 1 GAAGCAATCTGACATGCTGCCCTTCTCTCATGCTTGTCTGCTGTACAGCCCTGG 60
QY 79 aaatctgggagcagaatctgaagagcctctgcagagatctgtaaccacccctcga 138
    |||
Db 61 AAATCTGGAGAGCAAAATGAGACCTCTCCAGATCAGTACCAACACCTGCACCTT 120
QY 139 agtcatctgtagcccaacagaaatgagcctcctcctgctgctgtaagcaggaatg 198
    |||
Db 121 AGTCATCTGTACCCCAACAGAAATGCGCTGCTGCTGATGAGACGGATGGAGAGA 180
QY 199 aggtccacggggtgagaaggtgatacgaagctctgcagacctaagggtcctca 258
    |||
Db 181 AGGTCCACGGGGTGAGAAAGGTGATCCAGGTTGCCAGACCTATGGGGCTTCAGGTT 240
QY 259 gcaaggccctacaggtctcaatctggaacccaaggaagaaatgagcctcctg 318
    |||
Db 241 GCAGGCCCTACAGCTCCATGACCCAAAGAGAGAAATGCTCTGCGCCAACTGG 300
QY 319 accaaaggaggaacgtgactaaatgtaactccagacctccaaagatctcctgctc 378
    |||
Db 301 ACCAAAGGAGAAAGCTGACTAAGTGAACCTCCAGACTTCCAGTATCTCTGCTCAG 360
QY 379 tgggaagaagagtcctctctggaagcaggggaacatagacctccaaagcaaacag 438
    |||
Db 361 TGGGAAGAAGAGTCCCTCTCTGGAAAGCAGGGGAACATAGACCTCAAGCAACAGTCC 420
QY 439 taagaagagagctcgggcccagaagaagtaagtctcctcctgcaatgaaatctac 498
    |||
Db 421 TAAAGGAGAGCTT-GGCCCAAGAGAAAGTACGTCTCTGCTGCTACAG 478
QY 499 ggcgaagagctccacagagcccagaaggaagagagtgagcctcctgctgtaagagag 558
    |||
Db 479 GGC-AAAGGCTCCACAGGCCCCCAAGAGAAAGAGTGC---CCCTGCTTGCACGAGCCC- 533
QY 559 agggaaatgctggagcag 575
    |||
Db 534 -AGGAATGCTGAGACAG 549
```

RESULT 13  
BE308199 570 bp mRNA EST 26-OCT-2000  
601091376F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:3486019 5',  
DEFINITION  
MRA sequence.  
ACCESSION BE308199  
VERSION BE308199.1 GI:9164483  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 570)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov

Tissue Procurement: Lohar Hennighausen Ph.D., Robin Humphreys  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

Plate: LLAM5521 row: h column: 20  
High quality sequence stop: 554.  
Location/Qualifiers

FEATURES  
source

1..570

/organism="Mus musculus"  
/strain="C57/B6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3486019"  
/clone\_1ib="NCI\_CGAP\_Mam5"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-Sport6; Site.1: SalI;  
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigators  
providing samples: Lohar Hennighausen/Robin Humphreys,  
NIH"

BASE COUNT 151 a 140 c 185 g 94 t  
ORIGIN

Query Match 29.2%; Score 453.6; DB 166; Length 570;  
Best Local Similarity 98.1%; Pred. No. 3.6e-116;  
Matches 459; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```
QY 352 aggaattccagatattcctgtgcccagcttggaaagagctcctctggaagcagggaa 411
    |||
Db 1 AGGACTTCCAGAGTATCTGCTGCTCCAGCTGGGAAGAAAGTCCCTCTGGAAAGCAGGGAA 60
QY 412 catagacctcaagcaaaccaagctcctaaagagagctcggcccagaagagaatagg 471
    |||
Db 61 CATAGGACCTCAAGCAACCAAGCTCCTAAAGAGAGCTGGCCCAAGGAGAACTAGC 120
QY 472 tgctcctggaaatgaaagatctaaaggaggaaggtccaaaggtcccaaggagaag 531
    |||
Db 121 TGTCTCTGGCACTGCAAGGATCTTACAGGGGCAAAAGGCTCCACAGGCCCAAGGAGAAAG 180
QY 532 aggtgccctcgtgtgcaaggaagcccagaaggaatgctcggagcaagagacctgcggacc 591
    |||
Db 181 AGGTGCCCTGCTGTGCAAGAGAGCCCAAGGAATGCTGAGACACAGACACTGCGGACC 240
QY 592 tgcggtccacaaggaagctccaaaggtccaaaggagggcccacaggaactcaaggagga 651
    |||
Db 241 TGCGGCTCCACAGGAGACTCCAGTTCAGGGGGCCCCAGGACTCAAGGGGCAAGAGC 300
QY 652 tggtcctggagacagaggaatcaaaaggtgaaagcgggctccagaagctgctctgag 711
    |||
Db 301 TGTTCCTGGAGACAGAGGAATCAAAAGGTGAAGCGGCTTCACAGACTGCTGCTGAG 360
QY 712 gcaagcagctgagagccttaaaagaaactacagcgtctagaaggttgctctccacta 771
    |||
Db 361 GCAGCAGATGAGAGCCTTTAAAGAAAGAACTACAGCGTCTAGAGTTGCTCTCCACTA 420
QY 772 tcagaagagctgcatgtgtcctcgtatgagccatagaaggttgacaagaat 819
    |||
Db 421 TCAGAAAGCTGCATGTTCCCTCATGGCCGGAAGGTGTGAGACAAAGAT 468
```

RESULT 14  
BE916416 835 bp mRNA EST 29-SEP-2000  
601667002F1 NCI\_CGAP\_Mam1 Mus musculus cDNA clone IMAGE:3967032 5',  
DEFINITION  
MRA sequence.  
ACCESSION BE916416  
VERSION BE916416.1 GI:10417035  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 835)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

Plate: LLAM9141 row: c column: 01  
High quality sequence stop: 702.  
Location/Qualifiers

**SOURCE**

Query Match	27.6%	Score 428;	DB 141;	Length 835;
Best Local	80.0%	Pred. No. 6	5e-109;	
Matches 669;	Conservative	0;	Mismatch	0

[illegible]

QY	677	ggttaagcggcgcttcacagaacgtgcgtcctcttgagcagaatgtaagcccttaaaaga	736
Db	540	GGTAAAGCCGGCTTCCACACA - GGCTGTCTGAGCAGACAGATGAGAG - CTTAAAGGA	566
QY	737	aaactaagagctctagaggttgcctctcccatatcagaagaag - ctgaatcgttcacctga	795
Db	597	AAACTACAGCGCTCTGAGGTTG - CTTCTCCCACTATCAAAAAGCCCTGCATGTTCCCTGA	655
QY	796	tggccataagaagcttcgscagaatagaatgaagaagaaactctcatgaatgtttg	851
Db	656	TGGCGAAGCGTTTGGGACCAAGATCTTCAGGACACACAGACTGTGAAGAAGCTTTG	711

## RESULT 19

DEFINITION	663 bp	mRNA	EST	21-MAR-2001
ACCESSION	662502918p1	NIH_MGC_77	Homo sapiens cDNA clone	IMAGE:616381.5
VERSION	1			
KEYWORDS	mRNA sequence.			
SOURCE	RG482911			
ORGANISM	human.			

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1. *Strausberg, Barbara; Primates; Catarrhini; Hominoidea; Homo. (Bases 1 to 665)*  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

Email: c9apbs-remail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LINC1371 row: c column: 06  
High quality sequence stop: 655.  
Location/Qualifiers:

**FEATURES**  
**source**

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TMACE:4616381"
/clone_1lb="NH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: Lung; Vector: pNNR-LIB (Clontech); Site_1:
5'fl (ggcgcgttcggc); Site_2: 5'fl (ggcattatggc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGACC-3' and 3' adaptor sequence:
5'-ATTCTAGAGAGCGAGCGCCGACATC-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
BASE COUNT      149 a      180 c      241 g      94 t      1 others
ORIGIN

```

Query Match

Best Local Similarity	29.48;	score 3/8.6;	DB 154;	length 665;
Matches 487; Conservative	79.18;	Pred. NO. 4.3e-95;		
0; Mismatches 135				

33 Indels 4; Gaps 3;

[illegible]

109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400  
 401  
 402  
 403  
 404  
 405  
 406  
 407  
 408  
 409  
 410  
 411  
 412  
 413  
 414  
 415  
 416  
 417  
 418  
 419  
 420  
 421  
 422  
 423  
 424  
 425  
 426  
 427  
 428  
 429  
 430  
 431  
 432  
 433  
 434  
 435  
 436  
 437  
 438  
 439  
 440  
 441  
 442  
 443  
 444  
 445  
 446  
 447  
 448  
 449  
 450  
 451  
 452  
 453  
 454  
 455  
 456  
 457  
 458  
 459  
 460  
 461  
 462  
 463  
 464  
 465  
 466  
 467  
 468  
 469  
 470  
 471  
 472  
 473  
 474  
 475  
 476  
 477  
 478  
 479  
 480  
 481  
 482  
 483  
 484  
 485  
 486  
 487  
 488  
 489  
 490  
 491  
 492  
 493  
 494  
 495  
 496  
 497  
 498  
 499  
 500  
 501  
 502  
 503  
 504  
 505  
 506  
 507  
 508  
 509  
 510  
 511  
 512  
 513  
 514  
 515  
 516  
 517  
 518  
 519  
 520  
 521  
 522  
 523  
 524  
 525  
 526  
 527  
 528  
 529  
 530  
 531  
 532  
 533  
 534  
 535  
 536  
 537  
 538  
 539  
 540  
 541  
 542  
 543  
 544  
 545  
 546  
 547  
 548  
 549  
 550  
 551  
 552  
 553  
 554  
 555  
 556  
 557  
 558  
 559  
 560  
 561  
 562  
 563  
 564  
 565  
 566  
 567  
 568  
 569  
 570  
 571  
 572  
 573  
 574  
 575  
 576  
 577  
 578  
 579  
 580  
 581  
 582  
 583  
 584  
 585  
 586  
 587  
 588  
 589  
 590  
 591  
 592  
 593  
 594  
 595  
 596  
 597  
 598  
 599  
 600  
 601  
 602  
 603  
 604  
 605  
 606  
 607  
 608  
 609  
 610  
 611  
 612  
 613  
 614  
 615  
 616  
 617  
 618  
 619  
 620

55 aaacgaagagccctctcgcagagatcagtacccaacacctgcaccctagtcatgtgtagcc 152

110 AAATGAAGACCTACTCCACAGAACACGCCAGTGTTCACACCTGGTCAATGTGAGCT 169



**THIS PAGE BLANK (USPTO)**